



STIC Search Report

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STIC Database Tracking Number: 174856

TO: Chun Crowder
Location: rem/3B59/3C70
Art Unit: 1644
Wednesday, December 28, 2005
Case Serial Number: 10/780043

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Crowder,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1163.5	97.9	227	2	Q9UKJ0	HUMAN	Q9ukj0 homo sapien
2	973.5	81.9	203	2	Q9UKJ1	HUMAN	Q9ukj1 homo sapien
3	759	63.8	226	2	Q8NH11	HUMAN	Q8nh11 homo sapien
4	416	35.0	299	2	Q8BYA6	MOUSE	Q8bya6 mus musculus
5	128.5	10.8	823	1	AXL12	YEAST	P38928 saccharomyc
6	123.5	10.4	633	2	Q5W434	BRARE	Q5w434 brachydanio
7	123.5	10.4	651	2	Q5W433	BRARE	Q5w433 brachydanio
8	121	10.2	149	2	Q69YF9	HUMAN	Q69yfg homo sapien
9	121	10.2	271	1	Q9HBS0	HUMAN	Q9hbso homo sapien
10	116.5	9.8	275	2	Q41JC5	GIBBEZ	Q41jcs gibberella
11	110.5	9.3	245	2	Q65UQ5	MOUSE	Q65uq5 mus musculus
12	109.5	9.2	233	2	Q8TBC9	HUMAN	Q8tbc9 homo sapien
13	109.5	9.2	236	2	Q6PTQ7	HUMAN	Q6ptq7 homo sapien
14	108	9.1	397	1	GATV5	HUMAN	Q6bwx5 homo sapien
15	108	9.1	417	2	Q85VU4	HUMAN	Q85vu4 homo sapien
16	106	8.9	403	1	CD33	MOUSE	Q83994 mus musculus
17	105	8.8	442	2	Q9BY67	HUMAN	Q9by67 homo sapien
18	104	8.7	295	2	Q9Z2H8	MOUSE	Q9z2h8 mus musculus
19	104	8.7	445	2	Q8R4L1	MOUSE	Q8r4l1 mus musculus
20	103.5	8.7	359	2	Q5RLX6	RAT	Q5rlx6 rattus norv
21	103	8.7	233	2	Q6RJA3	HUMAN	Q6rja3 homo sapien
22	102	8.6	240	1	CD48	MOUSE	P18181 mus musculus
23	102	8.6	240	2	Q545K2	MOUSE	Q545k2 mus musculus
24	102	8.6	240	2	Q6P905	MOUSE	Q6p905 mus musculus
25	102	8.6	283	2	Q5DWN5	EPTBU	Q5dwn5 eptatretus
26	102	8.6	283	2	Q5DWN6	EPTBU	Q5dwn6 eptatretus
27	102	8.6	370	2	Q4KCS5	PSRP5	Q4kcs5 pseudomonas
28	101.5	8.5	151	2	Q8C2T1	MOUSE	Q8czt1 mus musculus
29	101.5	8.5	237	2	Q6DHW4	HUMAN	Q6dhw4 homo sapien
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Db 121 SVYFCRVELDTRRSGRQLOQSIKTKLTITQAVTTTTWRPSSTTTLAGRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVLTKTVIIGLLC-LLLMWRRRKGSRAPSSDF 226
Db 181 SWHLSLDTAIRVALAVLTKTVIIGLLC-LLLMWRRRKGSRAPSSDF 227

RESULT 2
Q9UKJ1 HUMAN
ID Q9UKJ1 HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PILRBeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD2964.1; -; mRNA.
DR Ensembl; ENSG00000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:000515; F:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADFCE80928B CRC64;

Query Match 81.9%; Score 973.5; DB 2; Length 303;
Best Local Similarity 82.5%; Pred. No. 1.9e-80;
Matches 188; Conservative 14; Mismatches 17; Indels 9; Gaps 2;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPKHLASMGGSVEIPFSFYYPWE 60
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Qy 121 SVYFCRVELDTRRSGRQLOQSIKTKLTITQAVTTTTWRPSSTTTLAGRV 172
Db 121 SVYFCRVELDTRRSGRQLOQSIKTKLTITQAVTTTTWRPSSTTTLAGRV 180
Qy 173 TESKGHSSWHLSDTAIRVALAVLTKTVIIGLLC-LLLMWRRRKGSR 220
Db 181 TQGRRSWSWHLSETAVGAVAVTVIIGLITGLICLLR-WRRRKGQ 227

RESULT 3
Q8NH11 HUMAN
ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH11;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PILRA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalek U., Smailus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RX Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017812; AAH17812.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;

Query Match 63.8%; Score 759; DB 2; Length 226;
Best Local Similarity 88.3%; Pred. No. 5.1e-61;
Matches 143; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

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Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LATAPDVRIWRGRGHFHGQSFYSTRPSPSIHKDYNNRFLFNWTEQSGSGLRISNLRKEDQ 120
Db 61 LATAPDVRIWRGRGHFHGQSFYSTRPSPSIHKDYNNRFLFNWTEQSGSGLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQLOQSIKTKLTITQAVTTTTWRPSS 162
Db 121 SVYFCRVELDTRRSGRQLOQSIKTKLTITQAVTTTTWRPSS 162

RESULT 4
Q8BYA6 MOUSE
ID Q8BYA6 MOUSE PRELIMINARY; PRT; 299 AA.
AC Q8BYA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630007P20 product:weakly similar to INHIBITORY
DE RECEPTOR PILRALPHA.
GN Name=Pilra; Synonyms=AV021745;
OS Mus musculus (Mouse).
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 23.5538 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-10
Perfect score: 1189
Sequence: 1 MGRPILLPILLPAPLQ.....LCLLLWRRKGRAPSSDF 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfilees1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1189	100.0	226	2	US-09-869-388-10
2	1163.5	97.9	227	2	US-09-869-388-6
3	1067	89.7	238	2	US-09-149-476-485
4	973.5	81.9	303	2	US-08-985-950-2
5	973.5	81.9	303	2	US-09-546-049-2
6	973.5	81.9	303	2	US-09-869-388-2
7	759	63.8	230	2	US-09-869-388-4
8	757.5	63.7	175	2	US-09-869-388-8
9	534	44.9	101	2	US-09-149-476-754
10	226	19.0	99	2	US-08-985-950-4
11	226	19.0	99	2	US-09-546-049-4
12	115.5	9.7	310	2	US-09-079-029-11
13	114.5	9.6	244	2	US-08-918-148-79
14	114.5	9.6	244	2	US-09-138-091A-77
15	114	9.6	352	2	US-09-203-958A-2
16	112	9.4	476	2	US-09-291-299A-3
17	109	9.2	143	1	US-08-345-321-8
18	107	9.0	355	2	US-08-875-811-57
19	105.5	8.9	622	1	US-08-356-786-16
20	105	8.8	440	2	US-09-866-028-61
21	105	8.8	440	2	US-09-944-457-61
22	105	8.8	440	2	US-09-945-584-61
23	105	8.8	440	2	US-09-944-944-61
24	105	8.8	440	2	US-09-945-587-61
25	105	8.8	442	2	US-09-778-510-20
26	105	8.8	442	2	US-09-930-803-1
27	104	8.7	265	1	US-08-403-853-16

28	104	8.7	423	2	US-09-778-510-22	Sequence 22, Appl
29	103	8.7	460	2	US-10-630-406-5	Sequence 5, Appl
30	102.5	8.6	421	2	US-08-759-628-5	Sequence 5, Appl
31	101.5	8.5	284	2	US-08-564-164A-2	Sequence 2, Appl
32	101.5	8.5	551	2	US-08-896-537A-2	Sequence 2, Appl
33	100	8.4	159	1	US-08-653-402B-2	Sequence 2, Appl
34	100	8.4	300	1	US-08-661-052-4	Sequence 4, Appl
35	100	8.4	300	2	US-09-188-082-4	Sequence 4, Appl
36	100	8.4	300	2	US-09-364-088-4	Sequence 4, Appl
37	100	8.4	300	2	US-09-102-716-4	Sequence 4, Appl
38	100	8.4	312	2	US-09-079-029-10	Sequence 10, Appl
39	100	8.4	354	2	US-09-393-627B-28	Sequence 28, Appl
40	100	8.4	360	2	US-09-907-794A-213	Sequence 213, App
41	100	8.4	360	2	US-09-905-125A-213	Sequence 213, App
42	100	8.4	360	2	US-09-902-775A-213	Sequence 213, App
43	100	8.4	360	2	US-09-906-700-213	Sequence 213, App
44	100	8.4	360	2	US-09-903-603A-213	Sequence 213, App
45	100	8.4	360	2	US-09-904-920A-213	Sequence 213, App

ALIGNMENTS

RESULT 1

US-09-869-388-10
; Sequence 10, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-10

Query Match 100.0%; Score 1189; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.4e-107;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGRPILLPILLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGSVEIPFSFYFWE 60
QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPSIHKDYVNRFLNWTGEGSGLRISNLKEDQ 120
DB 61 LATAPDVRIWRGRGHFGQSFYSTRPPSIHKDYVNRFLNWTGEGSGLRISNLKEDQ 120
QY 121 SVYFCRVELDTRRSRGRQQLQSIKGTKLITQAVTTTTTWRPSTTTIAGLRVTSKGHSE 180
DB 121 SVYFCRVELDTRRSRGRQQLQSIKGTKLITQAVTTTTTWRPSTTTIAGLRVTSKGHSE 180
QY 181 SWHLSLDTAIRVALAVAVLKVILGCLLLWRRKGRAPSSDF 226
DB 181 SWHLSLDTAIRVALAVAVLKVILGCLLLWRRKGRAPSSDF 226

RESULT 2

US-09-869-388-6
; Sequence 6, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel

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; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: S20977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 6
; LENGTH: 227
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-869-388-6

Query Match      97.9%; Score 1163.5; DB 2; Length 227;
Best Local Similarity 98.2%; Pred. No. 4.1e-105;
Matches 223; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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Db 61 LAIVPNVRIWRGHFPGQSYPSTRPPIHKDYVNRFLPLNWTGQSGFLRISNLRKEDQ 120

Qy 121 SVYFCRVELDTRRGRQQLQIKTKLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRGRQQLQIKTKLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180

Qy 181 SWHLSLDTAIRVALAVLKTIVILGLLC-LLLMWRRRKGSRAPSSDF 226
Db 181 SWHLSLDTAIRVALAVLKTIVILGLLC-LLLMWRRRKGSRAPSSDF 227

RESULT 3
US-09-149-476-485
; Sequence 485, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
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; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
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; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
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; EARLIER APPLICATION NUMBER: 60/047,615
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; EARLIER APPLICATION NUMBER: 60/047,597
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; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
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Result No.	Score	Query		Length	DB	ID	Description
		Match	\$				
1	114	9.6		250	6	US-10-512-184-27	Sequence 27, Appl
2	111	9.3		250	7	US-11-054-515-2073	Sequence 2073, Ap
3	110.5	9.3		256	7	US-11-054-515-907	Sequence 907, App
4	109	9.2		258	6	US-10-512-184-26	Sequence 26, Appl
5	109	9.2		327	6	US-10-512-184-62	Sequence 62, Appl
6	109	9.2		327	6	US-10-512-184-64	Sequence 64, Appl
7	109	9.2		328	6	US-10-512-184-63	Sequence 63, Appl
8	109	9.2		576	6	US-10-512-184-65	Sequence 65, Appl
9	109	9.2		625	6	US-10-512-184-47	Sequence 47, Appl
10	108.5	9.1		250	7	US-11-054-515-1319	Sequence 1319, Ap
11	108	9.1		250	7	US-11-054-515-2095	Sequence 2095, Ap
12	107.5	9.0		246	7	US-11-054-515-2079	Sequence 2079, Ap
13	106.5	9.0		252	7	US-11-054-515-897	Sequence 897, App
14	106.5	9.0		252	7	US-11-054-515-1016	Sequence 1016, Ap
15	106.5	9.0		252	7	US-11-054-515-1131	Sequence 1131, Ap
16	106.5	9.0		252	7	US-11-054-515-1135	Sequence 1135, Ap
17	106.5	9.0		252	7	US-11-054-515-1163	Sequence 1163, Ap
18	106.5	9.0		254	7	US-11-054-515-1893	Sequence 1893, Ap
19	106	8.9		242	7	US-11-054-515-1884	Sequence 1884, Ap
20	106	8.9		250	7	US-11-054-515-3247	Sequence 3247, Ap
21	105.5	8.9		252	7	US-11-054-515-1787	Sequence 1787, Ap
22	104.5	8.8		245	7	US-11-054-515-1346	Sequence 1346, Ap
23	104.5	8.8		247	7	US-11-054-515-1751	Sequence 1751, Ap
24	104.5	8.8		248	7	US-11-054-515-1617	Sequence 1617, Ap
25	104.5	8.8		251	7	US-11-054-515-1669	Sequence 1669, Ap

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 76.8906 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-10

Perfect score: 1189

Sequence: 1 MGRPILLPLLLLOPPAFLO.....LCILLWRRRKGRAPSDP 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1189	100.0	226	3	US-09-774-381-44
2	1189	100.0	226	4	US-10-780-043-10
3	1183	99.5	226	3	US-09-745-763-106
4	1163.5	97.9	227	4	US-10-262-445-128
5	1163.5	97.9	227	4	US-10-780-043-6
6	1163.5	97.9	227	5	US-10-820-474A-7
7	1163.5	97.9	291	3	US-09-935-390A-21
8	1163.5	97.9	226	4	US-10-276-774-2380
9	1067	89.7	238	3	US-09-809-391-485
10	1067	89.7	238	3	US-09-882-171-485
11	973.5	81.9	303	4	US-10-164-861-485
12	973.5	81.9	303	3	US-09-774-381-58
13	973.5	81.9	303	4	US-10-290-631-2
14	973.5	81.9	303	4	US-10-780-043-2
15	973.5	81.9	303	4	US-10-777-524-2
16	973.5	81.9	303	5	US-10-777-521-2
17	765	64.3	1012	5	US-10-450-763-30868
18	765	64.3	1012	5	US-10-450-763-33210
19	765	64.3	1012	5	US-10-450-763-47228
20	765	64.3	1012	5	US-10-450-763-51762
21	759	63.8	230	4	US-10-309-290-110
22	759	63.8	230	4	US-10-780-043-4
23	757.5	63.7	176	4	US-10-780-043-8
24	598	50.3	206	4	US-10-309-290-112
25	534	44.9	101	3	US-09-809-391-754
26	534	44.9	101	3	US-09-882-171-754
27	534	44.9	101	4	US-10-164-861-754

28	377	31.7	224	3	US-09-866-050A-711	Sequence 711, App
29	226	19.0	99	4	US-10-290-631-4	Sequence 4, Appli
30	226	19.0	99	4	US-10-777-524-4	Sequence 4, Appli
31	226	19.0	99	5	US-10-777-521-4	Sequence 4, Appli
32	122.5	10.3	257	4	US-10-270-073-8	Sequence 8, Appli
33	121.5	10.2	124	5	US-10-788-625-92	Sequence 92, Appli
34	121.5	10.2	253	4	US-10-479-670-174	Sequence 174, App
35	121.5	10.2	256	4	US-10-270-073-6	Sequence 6, Appli
36	116	9.8	252	4	US-10-479-670-168	Sequence 168, App
37	115.5	9.7	310	4	US-10-052-798-11	Sequence 11, Appl
38	115.5	9.7	310	4	US-10-288-917-11	Sequence 11, Appl
39	115.5	9.7	310	4	US-10-423-448-11	Sequence 11, Appl
40	115.5	9.7	448	4	US-10-378-567-2	Sequence 2, Appli
41	115	9.7	253	4	US-10-479-670-184	Sequence 184, App
42	114.5	9.6	244	5	US-10-778-394-77	Sequence 77, Appl
43	114.5	9.6	261	4	US-10-270-071-18	Sequence 18, Appli
44	114.5	9.6	261	4	US-10-270-073-2	Sequence 2, Appli
45	114.5	9.6	261	4	US-10-328-190-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-774-381-44
; Sequence 44, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-107CP2
; CURRENT APPLICATION NUMBER: US/09774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 44
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-381-44

Query Match 100.0%; Score 1189; DB 3; Length 226;
Best Local Similarity 100.0%; Pred. No. 8.5e-99;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPILLPLLLLOPPAFLOPGSGPSYLYGTQPHLSAKSGSVIEIFSPYFWE 60
|||||

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:18:33 ; Search time 94.0207 Seconds
(without alignments)
1056.147 Million cell updates/sec

Title: US-10-780-043-10

Perfect score: 1189

Sequence: 1 MGRPLLLPLLLLPPAPFLQ.....LCLLLWRRKGRAPSSDF 226

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1189	100.0	226	2	AAY08015 Human LSP
2	1189	100.0	226	2	AAB07447 A human m
3	1183	99.5	226	2	AAB080407 A secrete
4	1183	99.5	226	5	ABP61825 Human pol
5	1163.5	97.9	227	3	AAB07445 A human m
6	1163.5	97.9	227	6	ABU89824 TNF-recep
7	1163.5	97.9	291	2	AAB63682 Human sec
8	1163.5	97.9	326	4	ABBI2010 Human sec
9	1150.5	96.8	227	3	AAY87230 Human sig
10	1067	89.7	238	5	ABG95345 Human nov
11	1067	89.7	238	6	ABG034539 Region of
12	1067	89.7	238	7	AD123200 Novel hum
13	1067	89.7	238	8	ADH74202 Human sec
14	973.5	81.9	303	2	AAB62772 Human imm
15	973.5	81.9	303	3	AAB07443 A human m
16	973.5	81.9	303	8	ADP25129 PRO polyp
17	765	64.3	1012	4	ABG00509 Novel hum
18	765	64.3	1012	4	ABG16869 Novel hum
19	765	64.3	1012	4	ABG02851 Novel hum
20	765	64.3	1012	4	ABG21403 Novel hum
21	759	63.8	228	8	ADK98565 Human imm
22	759	63.8	230	3	AAB07444 A human m
23	759	63.8	230	7	ADE95578 Human NOV
24	757.5	63.7	175	3	AAB07446 A human m

25	598	50.3	206	7	ADE95580	Adc95580 Human NOV
26	534	44.9	101	2	AAW75053	AAW75053 Fragment
27	534	44.9	101	5	ABG95614	ABG95614 Human nov
28	534	44.9	101	6	ABO34808	ABO34808 Fragment
29	534	44.9	101	7	ADI23469	ADI23469 Novel hum
30	534	44.9	101	8	ADH74471	ADH74471 Human sec
31	377	31.7	224	5	ABE72387	ABE72387 Murine pr
32	369.5	31.1	212	2	ADE59537	ADE59537 Rat Prote
33	226	19.0	99	2	AAW62773	AAW62773 Partial m
34	122.5	10.3	257	6	ABR42758	ABR42758 Anti-CEA
35	122	10.3	565	4	AAI19873	AAI19873 Activatin
36	121.5	10.2	253	6	ABU97134	ABU97134 Recombina
37	121	10.2	256	6	ABR42757	ABR42757 Anti-CEA
38	121	10.2	271	5	AAU72792	AAU72792 Human ant
39	116.5	9.8	555	4	AAI19871	AAI19871 Activatin
40	116	9.8	252	6	ABU97128	ABU97128 Recombina
41	115.5	9.7	310	2	AAW83324	AAW83324 Single ch
42	115.5	9.7	310	5	ABB09605	ABB09605 Amino aci
43	115.5	9.7	310	6	ABG74386	ABG74386 Single ch
44	115.5	9.7	310	7	ADG98739	ADG98739 Human sin
45	115.5	9.7	310	8	ADO40448	ADO40448 Human sin

ALIGNMENTS

RESULT 1

AAY08015

ID AAY08015 standard; protein; 226 AA.

AC AAY08015;

DT 08-JUL-1999 (first entry)

DE Human LSP-1 protein.

KW LSP-1; signal peptide; leucocyte-specific protein-1; PA-I; TAP-1; cancer;
 KW proliferin analogue 1; thrombopoietin analogue protein 1; anticancer;
 KW antiangiogenic; anticancer; anti-inflammatory; anti-thrombocytopenic;
 KW anti-arthritis; signal transduction; inflammatory; disease; growth;
 KW proliferation; differentiation; cell survival; angiogenesis; diagnosis;
 KW haematopoietic stem cell; erythroid precursor; megakaryocytopoiesis;
 KW thrombopoiesis; prognosis; treatment; chromosome mapping; tissue typing;
 KW forensic; arthritis; thrombocytopenia; bone marrow transplant; infection;
 KW intravascular coagulation; iron deficiency; HIV; human.

OS Homo sapiens.

PN WO9918243-A1

XX 15-APR-1999

XX 06-OCT-1998; 98WO-US021151.

XX 06-OCT-1997; 97US-0061143P.

XX 06-OCT-1997; 97US-0061143P.

XX 06-OCT-1997; 97US-0061159P.

XX 08-JAN-1998; 98US-00004206.

XX 22-JAN-1998; 98US-00010674.

XX 27-JAN-1998; 98US-00014347.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Pan Y, Gearing DP, McCarthy SA;

XX WPI: 1999-264042/22.

XX N-PSDB; AAX37558.

XX Signal-peptide containing proteins that modulate cellular processes.

XX Claim 2; Fig 1; 124pp; English.

XX This invention describes the isolation of nucleic acids encoding the

CC signal-peptide-containing molecules leucocyte-specific protein-1 (LSP-1),
 CC proliferin analog I (PA-I) and thrombopoietin analog protein 1 (TAP-1).
 CC These proteins have antiangiogenic, anticancer, anti-inflammatory, anti-
 CC arthritic and anti-thrombocytopenic activity. The products of the
 CC inflammation and their modulators are involved in signal transduction,
 CC inflammatory responses, growth, proliferation, differentiation and
 CC survival of cells; angiogenesis; maturation of haematopoietic stem cells
 CC and erythroid precursors megakaryocytopoiesis and thrombopoiesis.
 CC Antibodies, or other binding agents, specific for the products of the
 CC invention are useful for diagnosis, prognosis and monitoring of treatment
 CC of diseases. Other uses include chromosome mapping, identification of
 CC individuals (tissue typing) and in forensic studies. LSP-1, PA-I and TAP-
 CC 1 proteins and nucleic acids are modulators of cellular processes,
 CC particularly they are used to treat or prevent diseases associated with
 CC deregulation of angiogenesis, immune responses and hematopoiesis, e.g.
 CC cancer, arthritis (and other inflammatory diseases), thrombocytopenia
 CC (caused by cancer treatment, bone marrow transplant, human immune
 CC deficiency virus infection etc.), intravascular coagulation, iron
 CC deficiency etc
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 XX Sequence 226 AA;

Query Match 100.0%; Score 1189; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.7e-95;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPQKHLASMGSGSVIIPPSFYYPWE 60
 DB 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPQKHLASMGSGSVIIPPSFYYPWE 60
 QY 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTQESGFLRISNLRKEDQ 120
 DB 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTQESGFLRISNLRKEDQ 120
 QY 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 DB 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 QY 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLMWRRRKGRAPSSDF 226
 DB 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLMWRRRKGRAPSSDF 226

RESULT 2
 AAB07447
 ID AAB07447 standard; protein; 226 AA.
 AC AAB07447;
 XX
 XX 20-OCT-2000 (first entry)
 DE A human monocyte-derived protein FDF03-S2.
 XX Human; monocyte-derived protein; FDF03; FDF03Daltatm; FDF03-S1;
 KW FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KW tissue rejection; inflammation; infection.
 XX
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..17
 FT /note= "signal sequence"
 FT Protein 18..226
 FT /note= "mature protein"
 XX WO200040721-A1.

XX 13-JUL-2000.
 XX 29-DEC-1999; 99WO-US030004.
 XX 31-DEC-1998; 98US-00223919.
 PR 31-DEC-1998; 98US-00224604.

XX (SCHE) SCHERING CORP.
 XX
 XX Bates E, Fournier N, Chaulus L, Garrone P;
 XX WPI; 2000-465984/40.
 DR N-PSDB; AAA58818.

XX Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
 PT diseases associated with changes in monocyte numbers, e.g. bacterial or
 FT viral infections.
 XX
 XX Claim 1; Page 41-42; 45pp; English.

XX The present sequence represents a human monocyte-derived protein. The
 CC specification describes monocyte-derived proteins FDF03, FDF03Daltatm,
 CC FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
 CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocyte-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocyte hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX Sequence 226 AA;

Query Match 100.0%; Score 1189; DB 3; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.7e-95;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPQKHLASMGSGSVIIPPSFYYPWE 60
 DB 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPQKHLASMGSGSVIIPPSFYYPWE 60
 QY 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTQESGFLRISNLRKEDQ 120
 DB 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTQESGFLRISNLRKEDQ 120
 QY 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 DB 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 QY 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLMWRRRKGRAPSSDF 226
 DB 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLMWRRRKGRAPSSDF 226

RESULT 3
 AAW80407
 ID AAW80407 standard; protein; 226 AA.

XX AAW80407;
 XX

DT 25-MAR-2003 (revised)
 DT 13-JAN-1999 (first entry)

XX A secreted protein encoded by clone di39_9.

XX Secreted protein; immune stimulating; suppressing;
 KW haematopoiesis regulating activity; tissue growth activity; activin;
 KW inhibit activity; chemotactic; chemokinetic activity; haemostatic;
 KW thrombolytic activity; anti-inflammatory activity; cadherin;
 KW tumour invasion suppressor activity; tumour inhibition activity.

XX Homo sapiens.
 XX WO9844113-A1.
 XX 08-OCT-1998.

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:18:33 ; Search time 72.8036 Seconds
(without alignments)
1056.147 Million cell updates/sec

Title: US-10-780-043-8
Perfect score: 934
Sequence: 1 MCRPLLLPLLLPAPFLQ.....KTQRSHMRISGMKQIKIIPS 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	934	100.0	175	3 AAB07446	Aab07446 A human m
2	821	87.9	303	2 AAW62772	Aaw62772 Human inm
3	821	87.9	303	3 AAB07443	Aab07443 A human m
4	821	87.9	303	8 ADP25129	Adp25129 PRO polyp
5	816	87.4	228	8 ADK98565	Adk98565 Human inm
6	816	87.4	230	3 AAB07444	Aab07444 A human m
7	816	87.4	230	7 ADP95578	Adp95578 Human NOV
8	809.5	86.7	1012	4 ABG00509	Abg00509 Novel hum
9	809.5	86.7	1012	4 ABG16869	Abg16869 Novel hum
10	809.5	86.7	1012	4 ABG02851	Abg02851 Novel hum
11	809.5	86.7	1012	4 ABG21403	Abg21403 Novel hum
12	757.5	81.1	226	2 AAW80407	Aaw80407 A secreta
13	757.5	81.1	226	2 AAY08015	Aay08015 Human LSP
14	757.5	81.1	226	3 AAB07447	Aab07447 A human m
15	757.5	81.1	226	5 ABP61825	Abp61825 Human pol
16	743.5	79.6	238	5 ABG95345	Abg95345 Human nov
17	743.5	79.6	238	6 AB034539	Ab034539 Region of
18	743.5	79.6	238	7 ADI23200	Adi23200 Novel hum
19	743.5	79.6	238	8 ADH74202	Adh74202 Human sec
20	742.5	79.5	227	3 AAB07445	Aab07445 A human m
21	742.5	79.5	227	6 ABU89824	Abu89824 TNF-recep
22	742.5	79.5	291	2 AAW63682	Aaw63682 Human sec
23	742.5	79.5	326	4 ABB12010	Abb12010 Human sec
24	729.5	78.1	227	3 AAY87230	Aay87230 Human sig

ALIGNMENTS

RESULT 1

AAB07446

ID AAB07446 standard; protein; 175 AA.

XX AC AAB07446;

XX DT 20-OCT-2000 (first entry)

XX DE A human monocyte-derived protein FDF03-M14.

XX KW Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1; FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia; tissue rejection; inflammation; infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..17

FT Protein /note= "signal sequence"

FT Protein 18..175

FT Protein /note= "mature protein"

XX PN WO200040721-A1.

XX XX 13-JUL-2000.

XX XX 29-DEC-1999; 99WO-US030004.

XX XX 31-DEC-1999; 98US-00223919.

XX XX 31-DEC-1999; 98US-00224604.

XX XX (SCHE) SCHERING CORP.

XX XX Bates E, Fournier N, Chaulus L, Garrone P;

XX XX WPI; 2000-465984/40.

XX XX N-PSDB; AAA58817.

XX XX Novel monocyte-derived polypeptides and polynucleotides, used to diagnose diseases associated with changes in monocyte numbers, e.g. bacterial or viral infections.

XX XX Claim 1; Page 39-40; 45pp; English.

XX The present sequence represents a human monocyte-derived protein. The specification describes monocyte-derived proteins FDF03, FDF03DeltaTM, FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the

CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocytic-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocytic hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX Sequence 175 AA;

Query Match 100.0%; Score 934; DB 3; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.4e-80;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPPLPAPLPQSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Db 1 MGRPLLLPPLPAPLPQSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPPSIHKDYVNRFLNWTGQKSGFLRISNLOKQDQ 120
 Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPSIHKDYVNRFLNWTGQKSGFLRISNLOKQDQ 120
 Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTQSHMRISGMKDKIQIPS 175
 Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTQSHMRISGMKDKIQIPS 175

RESULT 2

AAW62772
 ID AAW62772 standard; protein; 303 AA.

XX AAW62772;

DT 23-SEP-1998 (first entry)

XX Human immunoglobulin receptor designated FDF03.

XX Human; type I transmembrane protein; immunoglobulin-like domain; FDF03;
 KW activated monocyte; YE01; KTE03; control; development; differentiation;
 KW mammalian immune system; treatment; cancerous condition;
 KW degenerative condition; autoimmune response; transplantation rejection;
 KW graft versus host disease; inflammatory condition; detection; diagnosis;
 KW drug screening.

XX Homo sapiens.

XX WO9824906-A2.

XX 11-JUN-1998.

XX 05-DEC-1997; 97WO-US021101.

XX 06-DEC-1996; 96US-0032252P.

XX 09-DEC-1996; 96US-00762187.

XX 16-DEC-1996; 96US-0033181P.

XX 21-MAR-1997; 97US-0041279P.

XX (SCHE) SCHERING CORP.

XX Adema GJ, Maynard L, Gorman DM, Mcclanahan TK, Zurawski SM;

XX Zurawski G, Lanier LL, Phillips JH;

XX WPI; 1998-333325/29.

XX N-PSDB; AAV38987.

XX New isolated activated monocyte cell gene(s) - used to develop products

XX for treating e.g. cancer, degenerative conditions, autoimmune responses,

XX transplant rejection or inflammatory conditions.

XX The present sequence represents a human protein, FDF03, which is a type I
 CC transmembrane protein comprising an extracellular portion characterised
 CC by immunoglobulin-like domains, indicating that the protein is a receptor
 CC member of the immunoglobulin superfamily. The FDF03 gene is found in
 CC activated monocytes. The specification also describes other proteins
 CC encoded by activated monocytes, which are designated YE01 and KTE03. The
 CC genes function in controlling development, differentiation, and/or
 CC physiology of the mammalian immune system. The products can be used for
 CC treating abnormal proliferation, regeneration, degeneration or atrophy.
 CC They can be used for treating e.g. cancerous conditions, degenerative
 CC conditions, autoimmune responses, transplantation rejection, graft versus
 CC host disease, or inflammatory conditions. The products can also be used
 CC for detection, diagnosis and drug screening

XX Sequence 303 AA;

Query Match 87.9%; Score 821; DB 2; Length 303;
 Best Local Similarity 96.9%; Pred. No. 1.5e-69;
 Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRPLLLPPLPAPLPQSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Db 1 MGRPLLLPPLPAPLPQSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPPSIHKDYVNRFLNWTGQKSGFLRISNLOKQDQ 120
 Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPSIHKDYVNRFLNWTGQKSGFLRISNLOKQDQ 120
 Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTQ 159
 Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQAVTTTQ 159

RESULT 3

AAW07443

ID AAW07443 standard; protein; 303 AA.

XX AAW07443;

XX 20-OCT-2000 (first entry)

XX A human monocyte-derived protein FDF03.

XX Human; monocyte-derived protein; FDF03; FDF03deltaTM; FDF03-S1;
 KW FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KW tissue rejection; inflammation; infection.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 1..19

FT Peptide /note= "signal peptide"

FT Protein 20..303

FT /note= "mature protein"

XX WO2000040721-A1.

XX 13-JUL-2000.

XX 29-DEC-1999; 99WO-US030004.

XX 31-DEC-1998; 98US-00223919.

XX 31-DEC-1998; 98US-00224604.

XX (SCHE) SCHERING CORP.

XX Bates E, Fournier N, Chaulus L, Garrone P;

XX WPI; 2000-465984/40.

XX N-PSDB; AAA58814.

XX Novel monocyte-derived polypeptides and polynucleotides, used to diagnose

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:08 ; Search time 12.2093 Seconds
(without alignments)
1379.107 Million cell updates/sec

Title: US-10-780-043-8
Perfect score: 934
Sequence: 1 MGRPLLLPLPLLPAPFLQ.....KTQRSHWRISGMKDIQIPS 175

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	10.9	572	2 B46529	Ig Y heavy chain (
2	101.5	10.9	1694	2 S50065	sialoadhesin - mou
3	101	10.8	118	2 E27889	Ig heavy chain V r
4	100.5	10.8	151	2 I46626	rearranged T-cell
5	97	10.4	142	2 A28344	VpreB protein prec
6	97	10.4	392	2 B44194	poliovirus recepto
7	97	10.4	417	2 A44194	Ig lambda chain V-
8	96.5	10.3	110	2 S57442	Ig lambda chain -
9	96	10.3	235	2 S25758	VpreB protein prec
10	95.5	10.2	142	2 B28344	Ig light chain V r
11	94.5	10.1	132	2 A55410	T-cell receptor de
12	93.5	10.0	131	2 S36301	Ig lambda chain pr
13	93.5	10.0	132	2 PL0114	Ig lambda chain pr
14	93.5	10.0	132	2 S04937	Ig lambda chain V-
15	93.5	10.0	136	2 S16848	Ig heavy chain V r
16	93	10.0	119	2 D27889	MHC class II I-A-A
17	93	10.0	132	2 I71935	T-cell receptor de
18	93	10.0	142	2 S36316	m33-B isoform - mo
19	93	10.0	403	2 I52590	Ig lambda chain V-
20	92.5	9.9	111	1 L2HUBH	Ig light chain pre
21	92	9.9	125	2 A31493	secretory componen
22	92	9.9	773	1 ORBBG	T-cell receptor de
23	91.5	9.8	137	2 S36311	membrane-bound imm
24	91.5	9.8	226	2 A46477	Ig lambda chain V
25	91	9.7	112	2 S31515	Ig lambda chain pr
26	91	9.7	113	1 L1CHV	T-cell receptor de
27	91	9.7	145	2 S36299	Ig lambda chain pr
28	90.5	9.7	118	2 S04519	receptor tyrosine
29	90.5	9.7	882	2 I38912	

antibody light cha
Ig lambda chain V-
T-cell receptor de
Ig lambda chain pr
T-cell receptor de
T-cell receptor de
poliovirus recepto
poliovirus recepto
proteoglycan core
Ig lambda chain -
Ig kappa chain V r
rearranged T-cell
Ig heavy chain pre
Ig light chain var
Ig lambda chain -
Ig lambda chain V-

ALIGNMENTS

RESULT 1

B46529
Ig Y heavy chain (7.8S) - duck
N:Alternate names: Ig gamma chain (7.8S)
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A:Title: Structural relationship between the two IGY of the duck, Anas platyrhynchos: m
A:Reference number: B46529; MUID:93017865; PMID:1401901
A:Accession: B46529
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAG>
A:Cross-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:G62442; PIDN:CAA46322.1; PFI
A:Experimental source: spleen
A>Note: sequence extracted from NCBI backbone (NCBIP:116127)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 10.9%; Score 102; DB 2; Length 572;

Best Local Similarity 24.7%; Pred. No. 0.13;

Matches 40; Conservative 29; Mismatches 57; Indels 36; Gaps 8;

QY	5	L L L P L L L P A F L Q P S G T G S G P S Y L Y G V T Q P K H L S A S M G S V E I	-----P S F Y Y 57
DB	12	L L L A A V P G L R A A T L D E S G G	-----G G S L T L V C K G S G F T F S S Y G 55
QY	58	P W E L A T A P D V R I S W R R G --H F H G Q S F Y S T R P P S I H K D Y V N R L F L N W T E Q K S G F L R I S N L	115
DB	56	V S W V Q A F G K G L E W A G I T D S G S T Y Y A --P A V K ---G R T I S R N N G Q S T A T L Q M N S L	108
QY	116	Q K Q D S V T F C R V E L --D T R S G R Q Q W Q S I E G T K L S I T Q G N P S	155
DB	109	K A E D T A T Y C A K G A Y G I R S D I D L W G --H G T E V A V S G S P T	148

RESULT 2

S50065

sialoadhesin - mouse

C:Species: Mus musculus (house mouse)

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S50065

R:Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Mil

EMBO J. 13, 4490-4503, 1994

A:Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells

A:Reference number: S50065; MUID:95009950; PMID:7925291

A:Accession: S50065

A>Status: preliminary

A:Molecule type: mRNA

A/Residues: 1-1694 <CRO>
A/Cross-references: UNIPROT:Q62230; UNIPARC:UPI0000028B74; EMBL:Z36293; NID:G557253; PID

Query Match 10.9%; Score 101.5; DB 2; Length 1694;
Best Local Similarity 24.0%; Pred. No. 0.54;
Matches 31; Conservative 26; Mismatches 57; Indels 15; Gaps 4;
QY 33 YGVTPKHLASMGSGSVIPFSPYYPWELATAPDVRIWRGRGHFGQS-----FYSTRP 86
DB 21 WGVSPKRVQGLSGCLLIPCFYPADVPVSGITAIW-----YDYSGKQVVIHSGDP 76
QY 87 PSIHKDYVNRFLNWTGQSGFLRISNLQKQDSVYFCRVELDTRSSGRQWQSIETGK 146
DB 77 KLVDKRPGRGRLAGNMHDHVKCNLLKDLKPEDSDSYNFRFEI-----SDSNRLDVKGT 132
QY 147 LSITQGNPS 155
DB 133 VTVT-DPS 140

RESULT 3

E27889
Ig heavy chain V region (H18-8415) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: E27889
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a d
A/Reference number: A91043; MUID:86300658; PMID:2427335
A/Accession: E27889
A/Molecule type: DNA
A/Residues: 1-118 <CAT>
A/Cross-references: UNIPARC:UPI0000176B69
A/Experimental source: strain Balb/c
A/Note: This sequence was isolated from the germline gene
C/Comment: This chain was determined from a hybridoma protein that binds influenza virus h
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 101; DB 2; Length 118;
Best Local Similarity 24.8%; Pred. No. 0.023;
Matches 33; Conservative 25; Mismatches 35; Indels 40; Gaps 7;
QY 34 GVTQPKHLASMGSGVE-----IPFSPYYPWELATAPDVRIWRGRGHFGQSFYSTRP 86
DB 10 GLVKP-----GGSLKLSCAASGITFSDYMYVYRQTPDKRLW-----VATIT 52
QY 87 PSI---HKDYVNRFLNWTGQSGFLRISNLQKQDSVYFCRVELDTRSS-----GRQ 137
DB 53 DDINTYYSVDSVKGRFTISRDNAGNYYLQSLSKSEDTAMTC-----TRGSYYDYQMD 107
QY 138 QWQSIETGKLSIT 150
DB 108 YWG--QGTSTVTS 118

RESULT 4

I46626
rearranged T-cell receptor delta-chain/Vdelta.4-Ddelta.4 - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C/Accession: I46626
R/Jiang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A/Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A/Reference number: I46623; MUID:95363165; PMID:7636249
A/Accession: I46626
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-151 <YAN>
A/Cross-references: UNIPARC:UPI000011B2A5; GB:D49567; NID:G1041136; PIDN:BAA08511.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 10.8%; Score 100.5; DB 2; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.035;
Matches 39; Conservative 17; Mismatches 50; Indels 35; Gaps 4;
QY 6 LLPLLLPAPLQPSGSGSYLYGVTPKHLASMGSGSVIIPFSPYYPWELATAP 65
DB 3 LSSLLMLFLTSVP-----SGSGVAQKVQDQPV-VSRQGEAVTLNCRVTSWNETI- 54
QY 66 DVRIWRGRGHFGQSFYSTRPPIHKDYV-----NRLFLNWTGQSGFLRIS 113
DB 55 -----FWYKQPPSGEMTFLIYQYSASNAKGRVFINFQAKSLSLTIS 99
QY 114 NLQKQDSVYFCRVELDTRSS 134
DB 100 ALQLQDSATYFCALWVVVTMS 120

RESULT 5

A28344
VpreB protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C/Accession: A28344
R/Kudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A/Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se
A/Reference number: A91077; MUID:88029315; PMID:3117530
A/Accession: A28344
A/Molecule type: DNA
A/Residues: 1-142 <KUD>
A/Cross-references: UNIPROT:P13372; UNIPARC:UPI0000003EE4; GB:X05556; GB:Y00079; NID:G55
A/Note: the authors translated the codon GAG for residue 110 as Gln
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/20-142/Product: VpreB1 protein #status predicted <MAT>

Query Match 10.4%; Score 97; DB 2; Length 142;
Best Local Similarity 25.5%; Pred. No. 0.068;
Matches 41; Conservative 22; Mismatches 40; Indels 58; Gaps 8;
QY 12 LLLPAPLQPSGSGSYLYGVTPKHLASMGSGSVIIPFSPYYPWELATAPDVRIW 71
DB 7 LLMLLAVL-----TGCQPQM--VHQPPPLASSLGAT-----IRLSC 41
QY 72 RRGHFHQSFSYST-----RPSIHKDYVNRFLNWTGQ-----KS 107
DB 42 TLSNDHNIGIYIYVYQQRPGHPPR-----FLRYFHSKHKQDPDIPRFSGSKDTTRNL 97
QY 108 GFLRISNLQKQDSVYFCRVELDTRSSGR--QQWQSIETGK 146
DB 98 GYLISLQPEDEAVYYCAVGLRSQEKRMEREW---EGEK 135

RESULT 6

B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: B44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no puta
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: B44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-392 <KOI>
A/Cross-references: UNIPROT:P32506; UNIPARC:UPI000002B1F7; GB:S48817
C/Superfamily: poliovirus receptor; immunoglobulin homology
F/259-314/Domain: immunoglobulin homology <IMM>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 75.5168 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-8

Perfect score: 934

Sequence: 1 MGRPLLLPLLLPPAFLO.....KTQRSHMRISGMKDKIQIPS 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	821	87.9	303	Q9UKJ1_HUMAN	Q9ukj1 homo sapien
2	816	87.4	226	Q8NH11_HUMAN	Q8nh11 homo sapien
3	742.5	79.5	227	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
4	347	37.2	299	Q8BYA6_MOUSE	Q8bya6 mus musculus
5	121.5	13.0	633	Q5W434_BRACHYDANIO	Q5w434 brachydanio
6	121.5	13.0	633	Q5W433_BRACHYDANIO	Q5w433 brachydanio
7	109.5	11.7	233	Q8TBC9_HUMAN	Q8tbc9 homo sapien
8	103.5	11.1	235	Q6P2J1_HUMAN	Q6p2j1 homo sapien
9	102.5	11.0	149	Q69YF9_HUMAN	Q69yf9 homo sapien
10	102.5	11.0	271	Q9HBS0_HUMAN	Q9hbso homo sapien
11	102.5	11.0	400	Q4T054_TETNG	Q4t054 tetraodon n
12	101.5	10.9	1694	1 SN_MOUSE	Q62230 mus musculus
13	100.5	10.8	551	1 SIGL5_HUMAN	O15389 homo sapien
14	100	10.7	236	Q6PIQ7_HUMAN	Q6piq7 homo sapien
15	100	10.7	325	Q501V7_BRARE	Q501v7 brachydanio
16	97	10.4	142	1 VPRI1_MOUSE	P13372 mus musculus
17	97	10.4	142	Q5W1K4_MOUSE	Q5w1k4 mus musculus
18	97	10.4	142	Q545E0_MOUSE	Q545e0 m 13 days e
19	97	10.4	417	1 FV1_CERAE	P32506 cercopithec
20	96	10.3	302	Q4T853_TETNG	Q4t853 tetraodon n
21	96	10.3	328	Q6ZMC9_HUMAN	Q6zmc9 homo sapien
22	96	10.3	394	Q6UXG0_HUMAN	Q6uxg0 homo sapien
23	95.5	10.2	142	1 VPRE2_MOUSE	P13373 mus musculus
24	95.5	10.2	479	Q7TMK4_MOUSE	Q7tmk4 mus musculus
25	95	10.2	360	1 HPLN3_HUMAN	Q96886 homo sapien
26	95	10.2	595	2 Q5W431_FUGRU	Q5w431 fugu rubrip
27	95	10.2	630	2 Q5W436_FUGRU	Q5w436 fugu rubrip
28	95	10.2	648	2 Q5W435_FUGRU	Q5w435 fugu rubrip
29	95	10.2	1709	1 SN_HUMAN	Q9bzz2 homo sapien
30	95	10.2	1730	2 Q7YRQ7_PIG	Q7yrq7 sus scrofa
31	94.5	10.1	235	2 Q6FUG0_HUMAN	Q6pf90 homo sapien

32	94.5	10.1	358	2 Q7QAJ4_ANOGA	Q7qaj4 anopheles g
33	93.5	10.0	235	2 Q99M11_MOUSE	Q99m11 mus musculus
34	93.5	10.0	255	2 Q6KB05_MOUSE	Q6kb05 mus musculus
35	93.5	10.0	1035	2 Q6Q179_RAT	Q6q179 rattus norv
36	93	10.0	269	2 Q95KP8_PONPY	Q95kp8 pongo pygma
37	93	10.0	403	1 CD33_MOUSE	Q63994 mus musculus
38	92.5	9.9	111	1 LV2C_HUMAN	P01706 homo sapien
39	92.5	9.9	172	2 Q4TBU3_TETNG	Q4tbu3 tetraodon n
40	92.5	9.9	233	2 Q6GNH3_XENLA	Q6gnh3 xenopus lae
41	92	9.9	773	1 PIGR_RABIT	P01832 corytolagus
42	92	9.9	1032	1 CNT1A_BRARE	Q8axza brachydanio
43	91.5	9.8	226	1 CD79A_HUMAN	P11912 homo sapien
44	91	9.7	113	1 LVL_CHICK	P04210 gallus gall
45	91	9.7	236	2 Q6P5S3_HUMAN	Q6p5s3 homo sapien

ALIGNMENTS

RESULT 1

Q9UKJ1_HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2004 (Tremblrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127840; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
RT paired with the truncated counterparty PILRBeta.",
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD52964.1; -; mRNA.
DR Ensembl; ENSG00000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;

Query Match 87.9%; Score 821; DB 2; Length 303;
Best Local Similarity 96.9%; Pred. No. 1.5e-69;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	MGRPLLLPLLLPPAFLOPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Db	1	MGRPLLLPLLLPPAFLOPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
QY	61	LATAPDVRIWMRRGHFGHGSFYSTRPPSHKHQYVNRFLNWTGQKSGFLRISLNQKQDQ 120
Db	61	LATAPDVRIWMRRGHFGHGSFYSTRPPSHKHQYVNRFLNWTGQKSGFLRISLNQKQDQ 120
QY	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTQR 159
Db	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTQR 159

RESULT 2

Q8NH11_HUMAN

ID Q8NH1L HUMAN PRELIMINARY; PRT; 226 AA.
 AC Q8NH1L;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE PILRA protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RC Strausberg R.;
 RA Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017812; AAH17812.1; -; mRNA.
 DR InterPro; IPR003599; IG.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;

 Query Match 87.4%; Score 816; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 3e-69;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSPYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSPYFWE 60

 Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTQKSGFLRISLNQKODQ 120
 Db 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTQKSGFLRISLNQKODQ 120

 Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQG 152
 Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQG 152

 RESULT 3
 Q9UKJ0 HUMAN PRELIMINARY; PRT; 227 AA.
 ID Q9UKJ0;
 AC Q9UKJ0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Activating receptor PILRBeta (Hypothetical protein DKFZp4340079).

GN Name=DKFZp4340079;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
 RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.,
 RT "PILRBeta, a novel immunoreceptor tyrosine-based inhibitory motif-
 RT bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
 RT paired with the truncated counterpart PILRBeta.";
 RL J. Biol. Chem. 275:4467-4474 (2000).
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Testis;
 RC The German cDNA Consortium;
 RG Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.,
 RA Submitted (GEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION:
 CC O95870:BATS; NDExp=1; IntAct=EBI-347958, EBI-348517;
 DR EMBL; AF161081; AAD52965.1; -; mRNA.
 DR EMBL; AL834336; CAH10711.1; -; mRNA.
 DR IntAct; O9UKJ0; -;
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; NAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Hypothetical protein; Immunoglobulin domain; Receptor.
 KW SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;

 Query Match 79.5%; Score 742.5; DB 2; Length 227;
 Best Local Similarity 81.7%; Pred. No. 3e-62;
 Matches 143; Conservative 9; Mismatches 12; Indels 11; Gaps 2;

 Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSPYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSPYFWE 60

 Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTQKSGFLRISLNQKODQ 120
 Db 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTQKSGFLRISLNQKODQ 120

 Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQG-----NPSKTQRSHMRISGMK 168
 Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQAVTTTTPSPST----TTIAGLR 171

 RESULT 4
 Q8BYA6 MOUSE PRELIMINARY; PRT; 299 AA.
 ID Q8BYA6;
 AC Q8BYA6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A630007P20 product:weakly similar to INHIBITORY
 DE RECEPTOR PILRALPHA.
 GN Name=Pilra; Synonyms=AV021745;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Thymus;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 18.2386 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-8

Perfect score: 934

Sequence: 1 MGRPILLPLPPLPPAPLQ.....KTQRSHMRISGMKDKIQIPS 175

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgm2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgm2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgm2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgm2_6/ptodata/1/1aa/PCTUS COMB.pep.*
5: /cgm2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgm2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934	100.0	175	2	US-09-869-388-8
2	821	87.9	303	2	US-08-985-950-2
3	821	87.9	303	2	US-09-546-049-2
4	821	87.9	303	2	US-09-869-388-2
5	816	87.4	230	2	US-09-869-388-4
6	757.5	81.1	226	2	US-09-869-388-10
7	743.5	79.6	238	2	US-09-149-476-485
8	742.5	79.5	227	2	US-09-869-388-6
9	517	55.4	101	2	US-09-149-476-754
10	222	23.8	99	2	US-08-985-950-4
11	222	23.8	99	2	US-09-546-049-4
12	109.5	11.7	244	2	US-08-918-148-79
13	109.5	11.7	244	2	US-09-138-091A-77
14	100.5	10.8	551	2	US-08-896-537A-2
15	100	10.7	284	2	US-09-184-658-40
16	100	10.7	284	2	US-09-504-262D-40
17	98	10.5	355	2	US-08-875-811-57
18	97.5	10.4	104	2	US-10-083-424-40
19	97.5	10.4	553	1	US-08-661-052-16
20	97.5	10.4	553	2	US-09-188-082-16
21	97.5	10.4	553	2	US-09-364-088-16
22	97.5	10.4	553	2	US-09-102-716-16
23	95.5	10.2	421	2	US-08-759-628-5
24	95	10.2	143	1	US-08-345-321-8
25	95	10.2	360	2	US-09-907-794A-213
26	95	10.2	360	2	US-09-905-125A-213
27	95	10.2	360	2	US-09-902-775A-213

28	95	10.2	360	2	US-09-906-700-213	Sequence 213, App
29	95	10.2	360	2	US-09-903-603A-213	Sequence 213, App
30	95	10.2	360	2	US-09-904-920A-213	Sequence 213, App
31	95	10.2	360	2	US-09-909-064-213	Sequence 213, App
32	95	10.2	360	2	US-09-905-381A-213	Sequence 213, App
33	95	10.2	360	2	US-09-906-618-213	Sequence 213, App
34	95	10.2	360	2	US-09-906-646-213	Sequence 213, App
35	95	10.2	360	2	US-09-904-462-213	Sequence 213, App
36	95	10.2	360	2	US-09-903-736A-213	Sequence 213, App
37	95	10.2	360	2	US-09-906-722A-213	Sequence 213, App
38	95	10.2	1709	2	US-09-949-016-10503	Sequence 10503, A
39	94.5	10.1	126	2	US-08-751-359-11	Sequence 11, Appl
40	94.5	10.1	126	2	US-08-907-146-11	Sequence 11, Appl
41	94.5	10.1	262	2	US-09-069-821-4	Sequence 4, Appl
42	94.5	10.1	262	2	US-09-956-086-4	Sequence 4, Appl
43	94.5	10.1	262	2	US-09-956-087-4	Sequence 4, Appl
44	94.5	10.1	282	2	US-09-420-592A-7	Sequence 7, Appl
45	94.5	10.1	282	2	US-09-985-442-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-869-388-8

; Sequence 8, Application US/09869388

; Patent No. 6774214

; GENERAL INFORMATION:

; APPLICANT: Bates, Elizabeth

; APPLICANT: Fournier, Nathalie

; APPLICANT: Chalus, Lionel

; APPLICANT: Garrone, Pierre

; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METH

; FILE REFERENCE: SF0977X

; CURRENT APPLICATION NUMBER: US/09/869,388

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: IBM PC compatible

; SEQ ID NO 8

; LENGTH: 175

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-869-388-8

Query Match

Best Local Similarity 100.0%; Score 934; DB 2; Length 175;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPILLPLPPLPAPLQPSGTSGSPSYLYGTQPKHLSASMGSGVEIPFSYPWE 60

Db 1 MGRPILLPLPPLPAPLQPSGTSGSPSYLYGTQPKHLSASMGSGVEIPFSYPWE 60

QY 61 LATAPDVRISMRGHFHGQSFYSTRPPSIHKDYVNRFLNWTGEGKSGFLRISNLQKQDQ 120

Db 61 LATAPDVRISMRGHFHGQSFYSTRPPSIHKDYVNRFLNWTGEGKSGFLRISNLQKQDQ 120

QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTQRSHMRISGMKDKIQIPS 175

Db 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTQRSHMRISGMKDKIQIPS 175

RESULT 2

US-08-985-950-2

; Sequence 2, Application US/08985950

; Patent No. 6140076

; GENERAL INFORMATION:

; APPLICANT: Adema, Gosse Jan

; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,950
/ FILING DATE: 05-DEC-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/041,279
/ FILING DATE: 21-MARCH-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/033,181
/ FILING DATE: 16-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/032,252
/ FILING DATE: 06-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ching, Edwin P.
/ REGISTRATION NUMBER: 34,090
/ REFERENCE/DOCKET NUMBER: DX0670K
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650)852-9196
/ TELEFAX: (650)496-1204
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-985-950-2

Query Match 87.9%; Score 821; DB 2; Length 303;
Best Local Similarity 96.9%; Pred. No. 1.8e-77;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LATAPDVRISRRGHFHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120
Db 61 LATAPDVRISRRGHFHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120
Qy 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQGNPSKTQR 159
Db 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQAVTTTQR 159

RESULT 3
US-09-546-049-2
; Sequence 2, Application US/09546049
; Patent No. 6479638
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; Meyaard, Linde
; Gorman, Daniel M.
; McClanahan, Terrill K.
; Zurawski, Sandra M.
; Zurawski, Gerard
; Lanier, Lewis L.
; Phillips Jr., Joseph H.
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; Related Reagents
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto

/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/546,049
/ FILING DATE: 10-APR-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,950
/ FILING DATE: 05-DEC-1997
/ APPLICATION NUMBER: US 60/041,279
/ FILING DATE: 21-MARCH-1997
/ APPLICATION NUMBER: US 60/033,181
/ FILING DATE: 16-DEC-1996
/ APPLICATION NUMBER: US 60/032,252
/ FILING DATE: 06-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ching, Edwin P.
/ REGISTRATION NUMBER: 34,090
/ REFERENCE/DOCKET NUMBER: DX0670K
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650)852-9196
/ TELEFAX: (650)496-1204
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
/ US-09-546-049-2

Query Match 87.9%; Score 821; DB 2; Length 303;
Best Local Similarity 96.9%; Pred. No. 1.8e-77;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LATAPDVRISRRGHFHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120
Db 61 LATAPDVRISRRGHFHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120
Qy 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQGNPSKTQR 159
Db 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQAVTTTQR 159

RESULT 4
US-09-869-388-2
; Sequence 2, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-2

Result No.	Score	Query			DB	ID	Description
		Match	Length	Time			
1	934	100.0	175	4	US-10-780-043-8	Sequence 8, Appli	
2	821	87.9	303	3	US-09-774-381-58	Sequence 58, Appli	
3	821	87.9	303	4	US-10-290-631-2	Sequence 2, Appli	
4	821	87.9	303	4	US-10-780-043-2	Sequence 2, Appli	
5	821	87.9	303	4	US-10-777-524-2	Sequence 2, Appli	
6	821	87.9	303	5	US-10-777-521-2	Sequence 2, Appli	
7	816	87.4	230	4	US-10-309-290-110	Sequence 110, Appli	
8	816	87.4	230	4	US-10-780-043-4	Sequence 4, Appli	
9	809.5	86.7	1012	5	US-10-450-763-30868	Sequence 30868, A	
10	809.5	86.7	1012	5	US-10-450-763-33210	Sequence 33210, A	
11	809.5	86.7	1012	5	US-10-450-763-47228	Sequence 47228, A	
12	809.5	86.7	1012	5	US-10-450-763-51762	Sequence 51762, A	
13	757.5	81.1	226	3	US-09-745-763-106	Sequence 106, Appli	
14	757.5	81.1	226	3	US-09-774-381-44	Sequence 44, Appli	
15	757.5	81.1	226	4	US-10-780-043-10	Sequence 10, Appli	
16	743.5	79.6	238	3	US-09-809-391-485	Sequence 485, Appli	
17	743.5	79.6	238	3	US-09-882-171-485	Sequence 485, Appli	
18	743.5	79.6	238	4	US-10-164-861-485	Sequence 485, Appli	
19	742.5	79.5	227	4	US-10-262-445-128	Sequence 128, Appli	
20	742.5	79.5	227	4	US-10-780-043-6	Sequence 6, Appli	
21	742.5	79.5	227	5	US-10-820-474A-7	Sequence 7, Appli	
22	742.5	79.5	291	3	US-09-935-390A-21	Sequence 21, Appli	
23	742.5	79.5	326	4	US-10-276-774-2380	Sequence 2380, Appli	
24	655	70.1	206	4	US-10-309-290-112	Sequence 112, Appli	
25	517	55.4	101	3	US-09-809-391-754	Sequence 754, Appli	
26	517	55.4	101	3	US-09-882-171-754	Sequence 754, Appli	
27	517	55.4	101	4	US-10-164-861-754	Sequence 754, Appli	

;; TITLE OF INVENTION: AND USES THEREFOR
;; FILE REFERENCE: MNI-107CP2
;; CURRENT APPLICATION NUMBER: US/09/774,381
;; CURRENT FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: 08/941,354
;; PRIOR FILING DATE: 1999-09-30
;; PRIOR APPLICATION NUMBER: 09/010,674
;; PRIOR FILING DATE: 1998-01-22
;; PRIOR APPLICATION NUMBER: 60/061,149
;; PRIOR FILING DATE: 1997-10-06
;; PRIOR APPLICATION NUMBER: 09/014,347
;; PRIOR FILING DATE: 1998-01-27
;; PRIOR APPLICATION NUMBER: 60/061,159
;; PRIOR FILING DATE: 1997-10-06
;; PRIOR APPLICATION NUMBER: 09/474,151
;; PRIOR FILING DATE: 2000-12-21
;; PRIOR APPLICATION NUMBER: 09/004,206
;; PRIOR FILING DATE: 1998-01-08
;; PRIOR APPLICATION NUMBER: 60/061,143
;; PRIOR FILING DATE: 1997-10-06
;; PRIOR APPLICATION NUMBER: 09/483,414
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: 09/213,571
;; PRIOR FILING DATE: 1998-12-18
;; PRIOR APPLICATION NUMBER: 08/994,890
;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 59
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 58
;; LENGTH: 303
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-774-381-58

Query Match 87.9%; Score 821; DB 3; Length 303;
Best Local Similarity 96.9%; Pred. No. 6.5e-70;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGGSVEIPFSFYYPWE 60

Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTOR 159
Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQAVTTTQOR 159

RESULT 3

US-10-230-631-2

Sequence 2, Application US/102990631

Publication No. US20030105303A1

GENERAL INFORMATION:

APPLICANT: Adema, Gosse Jan

Meyard, Linde

Gorman, Daniel M.

McClanahan, Terrill K.

Zurawski, Sandra M.

Zurawski, Gerard

Lanier, Lewis L.

Phillips Jr., Joseph H.

TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;

Related Reagents

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESS: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

;; ZIP: 94304-1104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/290,631
;; FILING DATE: 08-No. US20030105303A1-2002.
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/985,950
;; FILING DATE: 05-DEC-1997
;; APPLICATION NUMBER: US 60/041,279
;; FILING DATE: 21-MARCH-1997
;; APPLICATION NUMBER: US 60/033,181
;; FILING DATE: 16-DEC-1996
;; APPLICATION NUMBER: US 60/032,252
;; FILING DATE: 06-DEC-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ching, Edwin P.
;; REGISTRATION NUMBER: 34,090
;; REFERENCE/DOCKET NUMBER: DX0670K
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 852-9196
;; TELEFAX: (650) 496-1204
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 303 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-290-631-2

Query Match 87.9%; Score 821; DB 4; Length 303;
Best Local Similarity 96.9%; Pred. No. 6.5e-70;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGGSVEIPFSFYYPWE 60

Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTOR 159
Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQAVTTTQOR 159

RESULT 4

US-10-780-043-2

Sequence 2, Application US/10780043

Publication No. US20040137506A1

GENERAL INFORMATION:

APPLICANT: Bates, Elizabeth

Fournier, Nathalie

APPLICANT: Chalus, Lionel

APPLICANT: Garone, Pierre

TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

FILE REFERENCE: SF0977X

CURRENT APPLICATION NUMBER: US/10/780,043

CURRENT FILING DATE: 2004-02-17

PRIOR APPLICATION NUMBER: US/09/869,388

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: IBM PC compatible

SEQ ID NO 2

LENGTH: 303

TYPE: PRT

ORGANISM: homo sapiens

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:41:30 ; Search time 3.31611 Seconds
(without alignments)
376.418 Million cell updates/sec

Title: US-10-780-043-8

Perfect score: 934

Sequence: 1 MGRPLLPLPLPLPPAPLQ.....KIQSHMRISGMKQIKIIPS 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	12.1	258	US-10-512-184-26	Sequence 26, Appl
2	113	12.1	327	US-10-512-184-62	Sequence 62, Appl
3	113	12.1	327	US-10-512-184-64	Sequence 64, Appl
4	113	12.1	328	US-10-512-184-63	Sequence 63, Appl
5	113	12.1	576	US-10-512-184-65	Sequence 65, Appl
6	113	12.1	625	US-10-512-184-47	Sequence 47, Appl
7	110.5	11.8	246	US-11-054-515-2077	Sequence 2077, Ap
8	110.5	11.8	246	US-11-054-515-2079	Sequence 2079, Ap
9	108.5	11.6	256	US-11-054-515-907	Sequence 907, Ap
10	106.5	11.4	250	US-10-512-184-27	Sequence 27, Appl
11	106	11.3	250	US-11-054-515-1319	Sequence 1319, Ap
12	106	11.3	258	US-11-054-515-1841	Sequence 1841, Ap
13	103	11.0	251	US-11-054-515-1827	Sequence 1827, Ap
14	102.5	11.0	250	US-11-054-515-1827	Sequence 3247, Ap
15	102.5	11.0	252	US-11-054-515-1021	Sequence 1021, Ap
16	102	10.9	245	US-11-054-515-1864	Sequence 1864, Ap
17	102	10.9	247	US-11-054-515-1751	Sequence 1751, Ap
18	102	10.9	250	US-11-054-515-837	Sequence 837, Ap
19	102	10.9	250	US-11-054-515-867	Sequence 867, Ap
20	102	10.9	250	US-11-054-515-1313	Sequence 1313, Ap
21	101.5	10.9	252	US-11-054-515-1787	Sequence 1787, Ap
22	100.5	10.8	242	US-11-054-515-1884	Sequence 1884, Ap
23	100.5	10.8	249	US-11-054-515-540	Sequence 540, Appl
24	100.5	10.8	254	US-11-054-515-1525	Sequence 1525, Ap
25	100.5	10.8	256	US-11-054-515-2080	Sequence 2080, Ap

ALIGNMENTS

RESULT 1

US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01

; CURRENT APPLICATION NUMBER: US/10/512,184

; CURRENT FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 26

; LENGTH: 258

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURES:

; OTHER INFORMATION: Description of Artificial Sequence: scFv CWPD2

; OTHER INFORMATION: with specificity against Fusarium spp.; originates

; OTHER INFORMATION: from Gallus gallus.

US-10-512-184-26

Query Match 12.1%; Score 113; DB 6; Length 258;

Best Local Similarity 31.5%; Pred. NO. 0.00048;

Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;

QY 23 GSTGSGPYLVGVTPKHLASMGSGSVIPSPS---FYYPW----ELATAPDVRIWRCH 75

Db 141 GSTKGAPA---LTQPSVSNALGTVEITCSGGYRGWFOQKSPGAPVTIYV---- 192

QY 76 FHQGSFYSTRPPSIHKDVVNLFLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132

Db 193 ---DDDSANRPSNIPSRP-----SGTSGSTATLTITGVQADDEAVYFGSY--DR 238

QY 133 SSGROQWQSIETKLSIT-QGNP 154

Db 239 SSG---YVSIFGAGTTLTVLGQP 258

RESULT 2

US-10-512-184-62

; Sequence 62, Application US/10512184

; Publication No. US20050244901A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

```

; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising AG - linker -
; OTHER INFORMATION: scFv CWP22.
US-10-512-184-62

Query Match      12.1%; Score 113; DB 6; Length 327;
Best Local Similarity 31.5%; Pred. No. 0.00064;
Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;

Qy 23 GSTGSGPSLYGVTPQKHLASMGSGVEIPPS---FYYPW---ELATAPDVRISWRGH 75
Db 210 GSTKGAPA---LTQPSVSANLGGTVEITCSGGYRYGWFQKSPGAPVTVIYW---- 261
Qy 76 FHGQSFYSTRPPIHDKYVNLPLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132
Db 262 ---DDDSANRSPNIPSRF-----SGTSGSTATLTITGVQADDEAVYFCGSY--DR 307
Qy 133 SSGRQMQSIEGTKLSIT-QGNP 154
Db 308 SSG---YVSIFGAGTTLTVLQGP 327

RESULT 3
US-10-512-184-64
; Sequence 64, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising lactoferricin - linker -
; OTHER INFORMATION: scFv CWP22.
US-10-512-184-64

Query Match      12.1%; Score 113; DB 6; Length 327;
Best Local Similarity 31.5%; Pred. No. 0.00064;
Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;

Qy 23 GSTGSGPSLYGVTPQKHLASMGSGVEIPPS---FYYPW---ELATAPDVRISWRGH 75
Db 210 GSTKGAPA---LTQPSVSANLGGTVEITCSGGYRYGWFQKSPGAPVTVIYW---- 261
Qy 76 FHGQSFYSTRPPIHDKYVNLPLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132
Db 262 ---DDDSANRSPNIPSRF-----SGTSGSTATLTITGVQADDEAVYFCGSY--DR 307
Qy 133 SSGRQMQSIEGTKLSIT-QGNP 154
Db 308 SSG---YVSIFGAGTTLTVLQGP 327

; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker -
; OTHER INFORMATION: scFv CWP22.
US-10-512-184-63

Query Match      12.1%; Score 113; DB 6; Length 328;
Best Local Similarity 31.5%; Pred. No. 0.00064;
Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;

Qy 23 GSTGSGPSLYGVTPQKHLASMGSGVEIPPS---FYYPW---ELATAPDVRISWRGH 75
Db 211 GSTKGAPA---LTQPSVSANLGGTVEITCSGGYRYGWFQKSPGAPVTVIYW---- 262
Qy 76 FHGQSFYSTRPPIHDKYVNLPLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132
Db 263 ---DDDSANRSPNIPSRF-----SGTSGSTATLTITGVQADDEAVYFCGSY--DR 308
Qy 133 SSGRQMQSIEGTKLSIT-QGNP 154
Db 309 SSG---YVSIFGAGTTLTVLQGP 328

RESULT 5
US-10-512-184-65
; Sequence 65, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising chitinase - linker -
; OTHER INFORMATION: scFv CWP22.
US-10-512-184-65

Query Match      12.1%; Score 113; DB 6; Length 576;
Best Local Similarity 31.5%; Pred. No. 0.0012;
Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;

Qy 23 GSTGSGPSLYGVTPQKHLASMGSGVEIPPS---FYYPW---ELATAPDVRISWRGH 75
Db 211 GSTKGAPA---LTQPSVSANLGGTVEITCSGGYRYGWFQKSPGAPVTVIYW---- 261
Qy 76 FHGQSFYSTRPPIHDKYVNLPLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132
Db 262 ---DDDSANRSPNIPSRF-----SGTSGSTATLTITGVQADDEAVYFCGSY--DR 307
Qy 133 SSGRQMQSIEGTKLSIT-QGNP 154
Db 308 SSG---YVSIFGAGTTLTVLQGP 327
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RESULT 4
US-10-512-184-63
; Sequence 63, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker -
; OTHER INFORMATION: scFv CWP22.
US-10-512-184-63

Query Match      12.1%; Score 113; DB 6; Length 328;
Best Local Similarity 31.5%; Pred. No. 0.00064;
Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;

Qy 23 GSTGSGPSLYGVTPQKHLASMGSGVEIPPS---FYYPW---ELATAPDVRISWRGH 75
Db 211 GSTKGAPA---LTQPSVSANLGGTVEITCSGGYRYGWFQKSPGAPVTVIYW---- 262
Qy 76 FHGQSFYSTRPPIHDKYVNLPLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132
Db 263 ---DDDSANRSPNIPSRF-----SGTSGSTATLTITGVQADDEAVYFCGSY--DR 308
Qy 133 SSGRQMQSIEGTKLSIT-QGNP 154
Db 309 SSG---YVSIFGAGTTLTVLQGP 328

RESULT 5
US-10-512-184-65
; Sequence 65, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising chitinase - linker -
; OTHER INFORMATION: scFv CWP22.
US-10-512-184-65

Query Match      12.1%; Score 113; DB 6; Length 576;
Best Local Similarity 31.5%; Pred. No. 0.0012;
Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;

Qy 23 GSTGSGPSLYGVTPQKHLASMGSGVEIPPS---FYYPW---ELATAPDVRISWRGH 75
Db 211 GSTKGAPA---LTQPSVSANLGGTVEITCSGGYRYGWFQKSPGAPVTVIYW---- 261
Qy 76 FHGQSFYSTRPPIHDKYVNLPLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132
Db 263 ---DDDSANRSPNIPSRF-----SGTSGSTATLTITGVQADDEAVYFCGSY--DR 308
Qy 133 SSGRQMQSIEGTKLSIT-QGNP 154
Db 309 SSG---YVSIFGAGTTLTVLQGP 328
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:41:30 ; Search time 4.30146 Seconds
(without alignments)
376.418 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPALLPLLLLLQPPAFLO.....CLLLWRRKGRAPSSDF 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

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- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	9.1	250	6	US-10-512-184-27
2	106.5	8.9	247	7	US-11-054-515-1294
3	106	8.9	250	7	US-11-054-515-2073
4	103.5	8.7	247	7	US-11-054-515-1328
5	103	8.6	250	7	US-11-054-515-2095
6	102.5	8.6	249	7	US-11-054-515-1030
7	102.5	8.6	252	7	US-11-054-515-897
8	102.5	8.6	252	7	US-11-054-515-1016
9	102.5	8.6	252	7	US-11-054-515-1131
10	102.5	8.6	252	7	US-11-054-515-1135
11	102.5	8.6	252	7	US-11-054-515-1163
12	102.5	8.6	253	7	US-11-054-515-902
13	102	8.6	258	6	US-10-512-184-26
14	102	8.6	327	6	US-10-512-184-62
15	102	8.6	327	6	US-10-512-184-64
16	102	8.6	328	6	US-10-512-184-63
17	102	8.6	576	6	US-10-512-184-65
18	102	8.6	625	6	US-10-512-184-47
19	101.5	8.5	256	7	US-11-054-515-907
20	100.5	8.4	254	7	US-11-054-515-1893
21	99.5	8.3	241	7	US-11-054-515-1911
22	99.5	8.3	250	7	US-11-054-515-1319
23	99	8.3	252	7	US-11-054-515-1549
24	98.5	8.3	246	7	US-11-054-515-2079
25	98.5	8.3	252	7	US-11-054-515-1145

ALIGNMENTS

RESULT 1

US-10-512-184-27
; Sequence 27, Application US/10512184
; Publication No. US2005024901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with
; OTHER INFORMATION: specificity against Fusarium spp.; originates from
; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

Query Match 9.1%; Score 109; DB 6; Length 250;
Best Local Similarity 29.5%; Pred. No. 0.0014;
Matches 33; Conservative 19; Mismatches 34; Indels 26; Gaps 5;
QY 21 PG-GSTGSPSYLYGVCTOPKHLASMGSGSVETPPSFYYPWELAIYVNVRISSHRGHFHCQ 79
DB 134 PEGSGTKGAPA---LTQPSVSANLGTGVTKITCS-----GSTAHYSHQKSPGS 180
QY 80 -----SFVSTRPSPSIHKDYVNRFLFNWTEGQESFLRISNLRKEDQSVYFC 125
DB 181 APVTLLISFNQRPSPDPSRF-----SGSKSGSTGLTITGVRAEDAVYVC 226

RESULT 2

US-11-054-515-1294
; Sequence 1294, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296

/ PRIOR FILING DATE: 2004-02-11
 / PRIOR APPLICATION NUMBER: 60/580,347
 / PRIOR FILING DATE: 2004-06-18
 / PRIOR APPLICATION NUMBER: 10/293,418
 / PRIOR FILING DATE: 2002-11-14
 / PRIOR APPLICATION NUMBER: 60/331,469
 / PRIOR FILING DATE: 2001-11-16
 / PRIOR APPLICATION NUMBER: 60/340,817
 / PRIOR FILING DATE: 2001-12-19
 / PRIOR APPLICATION NUMBER: 09/880,748
 / PRIOR FILING DATE: 2001-06-15
 / PRIOR APPLICATION NUMBER: 60/293,499
 / PRIOR FILING DATE: 2001-05-25
 / PRIOR APPLICATION NUMBER: 60/277,379
 / PRIOR FILING DATE: 2001-03-21
 / PRIOR APPLICATION NUMBER: 60/276,248
 / PRIOR FILING DATE: 2001-03-16
 / PRIOR APPLICATION NUMBER: 60/240,816
 / PRIOR FILING DATE: 2000-10-17
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 3247
 / SEQ ID NO 1294
 / LENGTH: 247
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-11-054-515-1294

 Query Match 8.9%; Score 106.5; DB 7; Length 247;
 Best Local Similarity 23.7%; Pred. No. 0.0023;
 Matches 52; Conservative 26; Mismatches 78; Indels 63; Gaps 8;

 QY 19 LOPGGSTGSGPSYLYGVTPQKHLASMGSGSVPEIPFSFYFPMELAIVPNVIRISW-----71
 DB 12 VXPGGSL-----RLSCAAG---FTSDYY-----MSWLRQAPGK 43
 QY 72 ---RGHPHGQSFYSTRPPSIHKVYVNLFLNWTGQSGFLRISNLRKEDQSVYFC-RV 127
 DB 44 GLERSVYISSSSYIYADVSK---GRFTISRDNAKNSLYLQMNLSRAEDTAVVYCARV 99
 QY 128 ELDTRESGRQQLQSIKGTGLTITQAVTTTTRPSSTTTIA---GLRVTESKHSESWHL 184
 DB 100 KRD-----ILTVGEVDVWGKTTVTSSGGGSGGGGGGGSGSEL 142
 QY 185 SLDTAIRVALAVLAKTVILGLCLLLWRRRKGSRAP 223
 DB 143 TQDPVAVSALGQTVRITCGGSLRSYASWYQKQGPAP 181

 RESULT 3
 US-11-054-515-2073
 / Sequence 2073, Application US/11054515
 / Publication No. US2005025532A1
 / GENERAL INFORMATION:
 / APPLICANT: Ruben et al.
 / TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 / FILE REFERENCE: PF523P3
 / CURRENT APPLICATION NUMBER: US/11/054,515
 / CURRENT FILING DATE: 2005-02-10
 / PRIOR APPLICATION NUMBER: 60/543,296
 / PRIOR FILING DATE: 2004-02-11
 / PRIOR APPLICATION NUMBER: 60/580,347
 / PRIOR FILING DATE: 2004-06-18
 / PRIOR APPLICATION NUMBER: 10/293,418
 / PRIOR FILING DATE: 2002-11-14
 / PRIOR APPLICATION NUMBER: 60/331,469
 / PRIOR FILING DATE: 2001-11-16
 / PRIOR APPLICATION NUMBER: 60/340,817
 / PRIOR FILING DATE: 2001-12-19
 / PRIOR APPLICATION NUMBER: 09/880,748
 / PRIOR FILING DATE: 2001-06-15
 / PRIOR APPLICATION NUMBER: 60/293,499
 / PRIOR FILING DATE: 2001-05-25
 / PRIOR APPLICATION NUMBER: 60/277,379
 / PRIOR FILING DATE: 2001-03-21
 / PRIOR APPLICATION NUMBER: 60/276,248
 / PRIOR FILING DATE: 2001-03-16
 / PRIOR APPLICATION NUMBER: 60/240,816
 / PRIOR FILING DATE: 2000-10-17
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 3247
 / SEQ ID NO 1328
 / LENGTH: 247
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-11-054-515-1328

 Query Match 8.7%; Score 103.5; DB 7; Length 247;
 Best Local Similarity 24.5%; Pred. No. 0.0045;
 Matches 47; Conservative 28; Mismatches 78; Indels 39; Gaps 8
 QY 46 GGSVEI-----PFSFYFPMELAIVPNVIRISW---RGHPFSGYSTRPPSIHKVYV 94

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 77.2308 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-6
Perfect score: 1192
Sequence: 1 MGRPLLLPLLLLLLQPPAFIQ.....CLLLWRRRKGRAPSSDP 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1192	100.0	227	4	US-10-262-445-128
2	1192	100.0	227	4	US-10-780-043-6
3	1192	100.0	227	5	US-10-820-474-7
4	1192	100.0	291	3	US-69-505-390A-3
5	1192	100.0	326	4	US-10-276-774-2380
6	1163.5	97.6	226	3	US-09-774-381-44
7	1163.5	97.6	226	4	US-10-780-043-10
8	1157.5	97.1	226	3	US-09-745-763-106
9	1069	89.7	238	3	US-09-809-391-485
10	1069	89.7	238	3	US-09-882-171-485
11	1069	89.7	238	4	US-10-164-861-485
12	958	80.4	303	3	US-09-774-381-58
13	958	80.4	303	4	US-10-290-631-2
14	958	80.4	303	4	US-10-780-043-2
15	958	80.4	303	4	US-10-777-524-2
16	958	80.4	303	5	US-10-777-521-2
17	752	63.1	1012	5	US-10-450-763-30868
18	752	63.1	1012	5	US-10-450-763-33210
19	752	63.1	1012	5	US-10-450-763-47228
20	752	63.1	1012	5	US-10-450-763-51762
21	744	62.4	230	4	US-10-309-290-110
22	744	62.4	230	4	US-10-780-043-4
23	742.5	62.3	175	4	US-10-780-043-8
24	592	49.7	206	4	US-10-309-290-112
25	532	44.6	101	3	US-09-809-391-754
26	532	44.6	101	3	US-09-882-171-754
27	532	44.6	101	4	US-10-164-861-754

28	370	31.0	224	3	US-09-866-050A-711	Sequence 711, Appl
29	223	18.7	99	4	US-10-290-631-4	Sequence 4, Appl
30	223	18.7	99	4	US-10-777-524-4	Sequence 4, Appl
31	223	18.7	99	5	US-10-777-521-4	Sequence 4, Appl
32	122	10.2	257	4	US-10-270-073-8	Sequence 8, Appl
33	120.5	10.1	256	4	US-10-270-073-6	Sequence 6, Appl
34	116.5	9.8	124	5	US-10-788-625-92	Sequence 92, Appl
35	116.5	9.8	253	4	US-10-478-670-174	Sequence 174, Appl
36	114	9.6	261	4	US-10-270-071-18	Sequence 18, Appl
37	114	9.6	261	4	US-10-270-073-2	Sequence 2, Appl
38	114	9.6	261	4	US-10-328-190-6	Sequence 6, Appl
39	112	9.4	352	3	US-09-203-958A-2	Sequence 2, Appl
40	112	9.4	352	5	US-10-764-131-2	Sequence 2, Appl
41	111	9.3	246	3	US-09-909-567B-49	Sequence 49, Appl
42	111	9.3	252	4	US-10-478-670-168	Sequence 168, Appl
43	110.5	9.3	310	4	US-10-052-798-11	Sequence 11, Appl
44	110.5	9.3	310	4	US-10-288-917-11	Sequence 11, Appl
45	110.5	9.3	310	4	US-10-423-448-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-262-445-128
; Sequence 128, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei

2n-1 = 128

2n = 129

POLYNUCLEOTIDES ENCODING THEM AND METHODS C

;; PRIOR FILING DATE: 2001-10-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 133
;; SOFTWARE: Curaseq1st version 0.1
;; SEQ ID NO 128
;; LENGTH: 227
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-262-445-128

Query Match 100.0%; Score 1192; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.6e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEQSGFLRISNLRKEDQ 120
Db 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEQSGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227

RESULT 2

US-10-780-043-6
;; Sequence 6, Application US/10780043
;; Publication No. US20040137506A1
;; GENERAL INFORMATION:
;; APPLICANT: Bates, Elizabeth
;; APPLICANT: Pournier, Nathalie
;; APPLICANT: Chalus, Lionel
;; APPLICANT: Garrone, Pierre
;; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
;; FILE REFERENCE: SF0977X
;; CURRENT APPLICATION NUMBER: US/10/780,043
;; PRIOR FILING DATE: 2004-02-17
;; PRIOR APPLICATION NUMBER: US/09/869,388
;; PRIOR FILING DATE: 2002-02-21
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: IBM PC compatible
;; SEQ ID NO 6
;; LENGTH: 227
;; TYPE: PRT
;; ORGANISM: homo sapiens
US-10-780-043-6

Query Match 100.0%; Score 1192; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.6e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEQSGFLRISNLRKEDQ 120
Db 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEQSGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227

RESULT 3

US-10-820-474A-7
;; Sequence 7, Application US/10820474A
;; Publication No. US20050155089A1
;; GENERAL INFORMATION:
;; APPLICANT: LAL, PREETI
;; APPLICANT: TANG, Y. TOM
;; APPLICANT: GORGONE, GINA A.
;; APPLICANT: CORLEY, NEIL C.
;; APPLICANT: GUEGLER, KARL J.
;; APPLICANT: BAUGHN, MARIAH R.
;; APPLICANT: AKERBLOW, INGRID E.
;; APPLICANT: AU-YOUNG, JANICE
;; APPLICANT: YUE, HENRY
;; APPLICANT: PATTERSON, CHANDRA
;; APPLICANT: REDDY, ROOPA
;; APPLICANT: HILLMAN, JENNIFER L.
;; APPLICANT: BANDMAN, OLGA
;; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
;; FILE REFERENCE: 039386-1568
;; CURRENT APPLICATION NUMBER: US/10/820,474A
;; PRIOR FILING DATE: 2004-04-07
;; PRIOR APPLICATION NUMBER: 09/720,533
;; PRIOR FILING DATE: 2001-03-20
;; PRIOR APPLICATION NUMBER: PCT/US99/14484
;; PRIOR FILING DATE: 1999-06-25
;; PRIOR APPLICATION NUMBER: 60/090,762
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/094,983
;; PRIOR FILING DATE: 1998-07-31
;; PRIOR APPLICATION NUMBER: 60/102,686
;; PRIOR FILING DATE: 1998-10-01
;; NUMBER OF SEQ ID NOS: 269
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 7
;; LENGTH: 227
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte Clone No: 962390
US-10-820-474A-7

Query Match 100.0%; Score 1192; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.6e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEQSGFLRISNLRKEDQ 120
Db 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEQSGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227

RESULT 4

US-09-935-390A-21
;; Sequence 21, Application US/09935390A
;; Patent No. US20020076761A1
;; GENERAL INFORMATION:
;; APPLICANT: Escobedo, Jaime
;; Quianjin, Hu

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1192	100.0	227	3	AA070445	A human m
2	1192	100.0	227	6	ABU89824	TNP-recep
3	1192	100.0	291	2	AAW63682	Human sec
4	1192	100.0	326	4	AAW612010	Human sec
5	1179	98.9	227	3	AAAY87230	Human sig
6	1163.5	97.6	226	2	AAAY08015	Human LSP
7	1163.5	97.6	226	3	AAW07447	A human m
8	1157.5	97.1	226	2	AAW80407	A secrete
9	1157.5	97.1	226	5	ABP61825	Human pol
10	1069	89.7	238	5	ABG95345	Human nov
11	1069	89.7	238	6	ABO34539	Region of
12	1069	89.7	238	7	ADT23200	Novel hum
13	1069	89.7	238	8	ADH74202	Human sec
14	958	80.4	303	2	AAW62772	Human imm
15	958	80.4	303	3	AAW07443	A human m
16	958	80.4	303	8	ADP25129	PRO poly
17	752	63.1	1012	4	ABG00509	Novel hum
18	752	63.1	1012	4	ABG16869	Novel hum
19	752	63.1	1012	4	ABG02851	Novel hum
20	752	63.1	1012	4	ABG21403	Novel hum
21	744	62.4	228	8	ADK98565	Human imm
22	744	62.4	230	3	AAW07444	A human m
23	744	62.4	230	7	ADP95578	Human NOV
24	742.5	62.3	175	3	AAW07446	A human m

CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocytic-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocytic hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 1192; DB 3; Length 227;
 Best Local Similarity 100.0%; Pred. No. 5e-97;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 DB 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 QY 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120
 DB 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120
 QY 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
 DB 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
 QY 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227
 DB 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227

RESULT 2
 ABU89824

ID ABU89824 standard; protein; 227 AA.

AC ABU89824;

DT 10-JUL-2003 (first entry)

DE TNF-receptor associated factor 5 (TRAF5) interacting protein #4.

KW Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;

KW TNF-receptor associated factor 5 interacting protein;

KW tumour necrosis factor associated factor 5 interacting protein;

KW TRAF5 interacting protein.

OS Homo sapiens.

XX WO20003031571-A2.

PD 17-APR-2003.

PF 02-OCT-2002; 2002WO-US031357.

XX 05-OCT-2001; 2001US-0327454P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328023P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0343629P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 25-JUN-2002; 2002US-0391342P.

PR 01-OCT-2002; 2002US-00262445.

XX (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
 PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;
 PI Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Spytek KA;
 PI Taupier RJ, Zehnusen BD, Zhong H, Zhong M;
 XX WPI; 2003-381704/36.
 DR N-PSDB; ACA90240.
 XX New DAPK3 polypeptide, useful for preparing a composition for treating or
 PT preventing e.g., cancer.
 XX Example 20F; Page 242; 253pp; English.

CC The invention describes an isolated polypeptide comprising any of 33 90-
 CC 1273 amino acid sequences (I) given in the specification or its mature
 CC form, a sequence that is at least 95 % identical to (I), or a sequence
 CC comprising one or more conservative substitutions in the amino acid
 CC sequence of (I). The polypeptide is useful for preparing a composition
 CC for treating or preventing e.g. cancer. This is the amino acid sequence
 CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
 CC interacting protein associated with the identification of novel human
 CC proteins and their functions

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 1192; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 5e-97;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 DB 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 QY 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120
 DB 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120
 QY 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
 DB 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
 QY 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227
 DB 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227

RESULT 3
 AAW63682

ID AAW63682 standard; protein; 291 AA.

AC AAW63682;

XX 24-SEP-1998 (first entry)

DT Human secreted protein 2.

DE Secreted protein; human; cell proliferation; cytokine activity; inhibin;
 KW tissue growth; cellular differentiation; regeneration; activin;
 KW chemotactic; haemostatic; thrombolytic; tumour inhibition;
 KW anti-inflammatory activity; biomarker.

OS Homo sapiens.

XX WO9825959-A2.

PN 18-JUN-1998.

PD 11-DEC-1997; 97WO-US022787.

PR 11-DEC-1996; 96US-0032757P.

XX (CHIR) CHIRON CORP.

XX

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:08 ; Search time 15.8372 Seconds
(without alignments)
1379.107 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPILLPLLLQLPPAFQLQ.....CLLLWRRKGRAPSSDF 227

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120.5	10.1	823	2 S48394	probable membrane
2	105.5	8.9	403	2 I52590	m33-B isoform - mo
3	104	8.7	1694	2 S50065	sialoadhesin - mou
4	103	8.6	240	2 JL0143	antigen BCM1 precu
5	101.5	8.5	392	1 RWHPD	poliovirus recepto
6	101.5	8.5	417	1 RWHPA	poliovirus recepto
7	100.5	8.4	478	2 I53960	PRR2 alpha - human
8	100.5	8.4	538	2 I68093	PRR2 delta - human
9	99	8.3	143	2 S36300	T-cell receptor de
10	99	8.3	210	2 E46482	T-cell surface gly
11	99	8.3	221	2 C46482	T-cell surface gly
12	99	8.3	246	2 D46482	T-cell surface gly
13	99	8.3	246	2 T01073	T cell surface gly
14	98.5	8.3	235	2 T14675	IG lambda chain -
15	98.5	8.3	772	2 T13078	KIAA0992 protein -
16	98	8.2	192	2 I33464	CD8 antigen - huma
17	98	8.2	210	2 S26657	T-cell surface gly
18	97	8.1	142	2 A28344	VpreB protein prec
19	96.5	8.1	1231	2 T18390	latrophilin-3, spl
20	96.5	8.1	1231	2 T18393	latrophilin-3, spl
21	96.5	8.1	1274	2 T18391	latrophilin-3, spl
22	96.5	8.1	1283	2 T18394	latrophilin-3, spl
23	96.5	8.1	1298	2 T18398	latrophilin-3, spl
24	96.5	8.1	1308	2 T18408	latrophilin-3, spl
25	96.5	8.1	1342	2 T18405	latrophilin-3, spl
26	96.5	8.1	1351	2 T18409	latrophilin-3, spl
27	96.5	8.1	1503	2 T18389	latrophilin-3, spl
28	96.5	8.1	1512	2 T18392	latrophilin-3, spl
29	96.5	8.1	1571	2 T18395	latrophilin-3, spl

30	96.5	8.1	1580	2 T18407	latrophilin-3, spl
31	96	8.1	392	2 B44194	poliovirus recepto
32	96	8.1	417	2 A44194	poliovirus recepto
33	95.5	8.0	145	2 S36299	T-cell receptor de
34	95	8.0	152	2 B26471	IG heavy chain pre
35	94	7.9	142	2 B28344	VpreB protein prec
36	93	7.8	122	2 H30535	IG heavy chain v r
37	92.5	7.8	119	2 D27889	IG heavy chain v r
38	92.5	7.8	132	2 P10114	IG lambda chain pr
39	92.5	7.8	142	2 S36310	T-cell receptor de
40	92	7.7	98	2 H47624	IG heavy chain v-I
41	91.5	7.7	213	2 A30585	T-cell surface gly
42	90.5	7.6	117	2 P10252	IG heavy chain v r
43	90.5	7.6	213	2 A34953	T-cell surface gly
44	90.5	7.6	710	2 A39486	ABC transporter, b
45	90.5	7.6	735	2 S76425	hypothetical prote

ALIGNMENTS

RESULT 1

S48394

probable membrane protein Y1L140w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004

C:Accession: S48394; S50276

R:Churcher, C.

submitted to the EMBL Data Library, September 1994

A:Reference number: S48310

A:Accession: S48394

A:Molecule type: DNA

A:Residues: 1-823 <CHU>

A:Cross-references: UNIPROT:P38928; UNIPARC:UPI000012669C; GB:Z47047; EMBL:Z38059; NID:9

R:Torpey, L.E.; Gibbs, P.E.M.; Nelson, J.; Lawrence, C.W.

Yeast 10, 1503-1509, 1994

A:Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-

A:Reference number: S50275; MUID:95176709; PMID:7871890

A:Accession: S50276

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 80-823 <TOR>

A:Cross-references: UNIPARC:UPI00001689D0; EMBL:U07228; NID:G460247; PIDN:AAA67919.1; P1

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994

C:Genetics:

A:Gene: SGD:SRO4

A:Cross-references: SGD:S0001402; MIPS:Y1L140w

A:Map position: 9L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein Y1L140w

C:Keywords: transmembrane protein

F16-22/Domain: transmembrane #status predicted <TM1>

F1511-527/Domain: transmembrane #status predicted <TM2>

Query Match 10.1%; Score 120.5; DB 2; Length 823;
Best Local Similarity 23.0%; Pred. No. 0.022; Matches 60; Conservative 43; Mismatches 85; Indels 73; Gaps 15;

QY 12 LLQPPAFIQPGST--GSGPSYLYGV-TQPKHLSASM---GGSVEIPFSFYFWE-----60

Db 293 LLDAPDWALDNATISGSPVDELLGKSNPNANFSVIYDTYGDV-----IYFNFVWSTT 347

QY 61 ----LAIYVNVRIISWRGHFGQSPYSTRPISIHKDYVNR-----LFLN-----WTEGQE 106

Db 348 DLFAISLSLFINAT--RGEWFSYFLP-----PSQFTDYVNTVNSLFTNSSQDHDWVKFOS 401

QY 107 S-----GFLRIS-----NLKEDOSVYFCVELDTR-----BSGRQQ 138

Db 402 SNLTAGVPPKPNFDKSLGLKANQSQSQCELYFNIGMDSKLTTHNSHANATSTSSSHHS 461

QY 139 LQSIGKGTLLTTOAVTTTTTWRPSTTTIAGLRVTFESKGHSWMHLSLDTAIRVALAVAV 198

Db 462 TSTSTSTSTYTAKISSISA-AATSSAPALPAANKTSSHVK-----AVAIACGVAI 513

```
Qy 199 -LKTIVLGLCLLMLWRRK 218
      : : : : :
Db 514 PLGVILVALICFLIFWRRRE 534
      : : : : :

RESULT 2
152590
m33-B isoform - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: 152590
Blood 83, 3188-3198, 1994
A:Title: Molecular cloning of two isoforms of the murine homolog of the myeloid CD33 and
A:Reference number: 152590, MUID:94250900; PMID:8193354
A:Accession: 152590
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-403 <RES>
A:Cross-references: UNIPARC:UPI0000020E12; GB:S71345; NID:G551352; PIDN:AA830842.1; PID:
      8.9%; Score 105.5; DB 2; Length 403;
Query Match Best Local Similarity 21.8%; Pred. No. 0.18;
Matches 63; Conservative 36; Mismatches 103; Indels 87; Gaps 10;

Qy 5 LLLPLLLLOPPAFLOPGSGTSGPSYLYGVTPQKHLASMGSGSVPEIPFSPYYPWEIAIV 64
      : : : : :
Db 1 MLWFL-----PLFLCAGSLAQ--DLEFQVLAESVTVVEGLCVHVPSCVFPYSIKLTL 52
      : : : : :

Qy 65 PNVRISM-RRG-HFHGQSFYSTRPPS--IHKDYVNRFLFNWTEQSGGFLRISNRKEDQ 120
      : : : : :
Db 53 GPVTGMLRKGVLHEDSPVATSDPRLQVQKATQGRFQLGDPQKHDCSLFIRDAQKNDT 112
      : : : : :

Qy 121 SVYFCRV--ELDTRSGRQOQSIKGYKLTIT-----QA 152
      : : : : :
Db 113 GMYFRRVREPFVRSYKKSQLSLHVTLSLSTPDIIIPGLEAGYPSNLTCSPWACEQG 172
      : : : : :

Qy 153 VTTTWRPSTTTIAG-----LRVT 173
      : : : : :
Db 173 TPPTFSWMSTALTSLSRTDSSVLTFPTPQDQHGKTKLCTLVTSAGAVTVERTIQLNVT 232
      : : : : :

Qy 174 ESKGHSEWHLSLTAIRVALAVLKVILGL-LCLLLWRRRKGRS 221
      : : : : :
Db 233 RKSG-----QMRELVLAVGEATVKLLILGLCLVFLVNFCKRRTTK 274
      : : : : :

RESULT 3
S50065
sialoadhesin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S50065
R:Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Mill
EMBO J. 13, 4490-4503, 1994
A:Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells
A:Reference number: S50065; MUID:95009950; PMID:7925291
A:Accession: S50065
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1694 <CRO>
A:Cross-references: UNIPROT:Q62230; UNIPARC:UPI0000028B74; EMBL:Z36293; NID:G557253; PID:
      8.7%; Score 104; DB 2; Length 1694;
Query Match Best Local Similarity 22.7%; Pred. No. 1.3;
Matches 53; Conservative 32; Mismatches 92; Indels 56; Gaps 8;

Qy 5 LLLPLLLLOPPAFLOPGSGTSGPSYLYGVTPQKHLASMGSGSVPEIPFSPYYPWEIAIV 64
      : : : : :
Db 3 VLPSLLL-----ASVPSLGQTGWSSPNVQGLSGSLIICIESPADVPVS 52
      : : : : :

Qy 65 PNVRISMRRGHFHGQS-----FYSTRPPSIHKDYVNRFLFNWTEQSGGFLRISNRK 118
      : : : : :
Db 53 NGITAIW----YDYSGRQVVIHSGDPKLVDRPGRGAELMGNMDHKVCNLLKDLKPE 108
      : : : : :
```

```
Qy 119 DQSVYFCRVELDTRRSGRQOQSIKGYKLTITQAVTTTTTWRPSSSTTIAGLRVTSKGH 178
      : : : : :
Db 109 DSGTYNFRFEI-----SDSNRLVDVKG-----TVVTDDPSPTTITPELR-----EGM 154
      : : : : :

Qy 179 SESWHLSLDTAIRVALAVLKVILGLLCL-----LLLWRRRKGRAPSSDF 227
      : : : : :
Db 155 ERNPNCTP-----YLCLEKQVSLQWRGQDPTHVTSSTP 189
      : : : : :
```

RESULT 4

```
Qy 119 DQSVYFCRVELDTRRSGRQOQSIKGYKLTITQAVTTTTTWRPSSSTTIAGLRVTSKGH 178
      : : : : :
Db 109 DSGTYNFRFEI-----SDSNRLVDVKG-----TVVTDDPSPTTITPELR-----EGM 154
      : : : : :

Qy 179 SESWHLSLDTAIRVALAVLKVILGLLCL-----LLLWRRRKGRAPSSDF 227
      : : : : :
Db 155 ERNPNCTP-----YLCLEKQVSLQWRGQDPTHVTSSTP 189
      : : : : :

antigen BCM1 precursor - mouse
N:Alternate names: CD48 antigen homolog agp-60; OX45 antigen, Blast-1 antigen
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JLO143; S21319; A47469; B47469
R:Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A:Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1)
region on mouse chromosome 3.
A:Reference number: JLO143; MUID:90278362; PMID:1693656
A:Accession: JLO143
A:Molecule type: mRNA
A:Residues: 1-240 <MON>
A:Cross-references: UNIPROT:P18181; UNIPARC:UPI0000003EBF; EMBL:X17501; NID:G50134; PIDN:
R:Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seidin, M.F.
submitted to the EMBL Data Library, June 1990
A:Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blast-1)
3 region on mouse chromosome 3.
A:Reference number: S21319
A:Accession: S21319
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-240 <MON2>
A:Cross-references: UNIPARC:UPI0000003EBF; EMBL:X53526; NID:G50138; PIDN:CAA37604.1; PID
R:Cabrero, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 3418-3422, 1993
A:Title: Identification, by protein sequencing and gene transfection, of agp-60 as the m
A:Reference number: A47469; MUID:93234508; PMID:8475091
A:Accession: A47469
A:Molecule type: protein
A:Residues: 74-80 <CAB>
A:Cross-references: UNIPARC:UPI0000176785
A:Experimental source: EL-4 lymphoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:129658)
A:Accession: B47469
A:Molecule type: protein
A:Residues: 84-98 <CA2>
A:Cross-references: UNIPARC:UPI0000176786
A:Experimental source: EL-4 lymphoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:129660)
C:Comment: This antigen is widely expressed on leukocytes and is likely to be anchored t
C:Superfamily: B-cell surface glycoprotein blast-1
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-217/Product: antigen BCM1 #status predicted <MAT>
F:218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F:32,38,70,136,186,203/Binding site: carboxylate (Asn) (covalent) #status predicted
F:217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
```

```
Query Match 8.6%; Score 103; DB 2; Length 240;
Best Local Similarity 23.6%; Pred. No. 0.16;
Matches 45; Conservative 33; Mismatches 63; Indels 50; Gaps 9;
```

```
Qy 5 LLLPLLLLOPPAFLOPGSGTSGPSYLYGVTPQKHLASMGSGSVPEIPFSPYYPWEIAIV 64
      : : : : :
Db 10 LVLELLL-----PLGTGFGQHSI-----PDNATTSNVLEKIH-----KDPLG 49
      : : : : :

Qy 65 PNVRISMRRGHFHGQS-----YSTRPPSIHKDYVNRFLFNWTEQSGGFLRISNRKEDQ 120
      : : : : :
Db 50 PYKRITWL--HTKNQKILEYVNSTKTIFSEFGRVYLE-----ENNGLHISNVRKEDK 103
      : : : : :
```


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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 97.9561 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPLLLLLLLLLQPPAFLO.....CLLLWRRRKSRAPSSDP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1192	100.0	227	Q9UKJ0 HUMAN	Q9ukj0 homo sapien
2	998	80.4	303	Q9UKJ1 HUMAN	Q9ukj1 homo sapien
3	744	62.4	226	Q8NH11 HUMAN	Q8nh11 homo sapien
4	410	34.4	299	Q8BYA6 MOUSE	Q8bya6 mus musculus
5	123.5	10.4	633	Q5W434 BRARE	Q5w434 brachydanio
6	123.5	10.4	651	Q5W433 BRARE	Q5w433 brachydanio
7	120.5	10.1	823	AXL2 YEAST	P38928 saccharomyc
8	118	9.9	149	Q69YF9 HUMAN	Q69yf9 homo sapien
9	118	9.9	271	Q9HBS0 HUMAN	Q9hbso homo sapien
10	115.5	9.7	831	Q755V1 ASHGO	Q755v1 ashbya goss
11	111	9.3	275	Q41JC5 GIBZE	Q41jc5 gibberella
12	107.5	9.0	442	Q9BY67 HUMAN	Q9by67 homo sapien
13	106.5	8.9	295	Q9Z2H8 MOUSE	Q9z2h8 mus musculus
14	106.5	8.9	445	Q8K4L1 MOUSE	Q8k4l1 mus musculus
15	105.5	8.9	403	CD33 MOUSE	Q63994 mus musculus
16	104	8.7	1694	SN MOUSE	Q62230 mus musculus
17	103.5	8.7	233	Q8TBC9 HUMAN	Q8tbc9 homo sapien
18	103.5	8.7	369	Q7YUQ4 9TRYP	Q7yuq4 trypanosoma
19	103.5	8.7	445	Q8K3T6 MOUSE	Q8k3t6 mus musculus
20	103	8.6	240	CD48 MOUSE	P18181 mus musculus
21	103	8.6	240	Q545K2 MOUSE	Q545k2 mus musculus
22	103	8.6	240	Q6P905 MOUSE	Q6p905 mus musculus
23	103	8.6	397	GATA5 HUMAN	Q9bwx5 homo sapien
24	103	8.6	417	Q86VU4 HUMAN	Q86vu4 homo sapien
25	102.5	8.6	151	Q8C2T1 MOUSE	Q8c2t1 mus musculus
26	102.5	8.6	283	Q5DMN5 EPTBU	Q5dmn5 eptatretus
27	102.5	8.6	283	Q5DMN6 EPTBU	Q5dmn6 eptatretus
28	102.5	8.6	369	Q7YUQ1 9TRYP	Q7yuq1 trypanosoma
29	101.5	8.5	359	Q5R1X6 RAT	Q5r1x6 rattus norv
30	101.5	8.5	369	Q7YUQ2 9TRYP	Q7yuq2 trypanosoma
31	101.5	8.5	370	Q4KCC5 PSERF5	Q4kcc5 pseudomonas

32	101.5	8.5	417	1	PVR HUMAN	P15151 homo sapien
33	101.5	8.5	595	2	Q5W431 FUGRU	Q5w431 fugu rubrip
34	101.5	8.5	630	2	Q5W436 FUGRU	Q5w436 fugu rubrip
35	101.5	8.5	648	2	Q5W435 FUGRU	Q5w435 fugu rubrip
36	100.5	8.4	236	2	Q6PIQ7 HUMAN	Q6piq7 homo sapien
37	100.5	8.4	347	2	Q60H11 EPTBU	Q60h11 eptatretus
38	100.5	8.4	369	2	Q7YUQ3 9TRYP	Q7yuq3 trypanosoma
39	100.5	8.4	479	2	Q61B16 HUMAN	Q61b16 homo sapien
40	100.5	8.4	538	1	PVR2 HUMAN	Q92692 homo sapien
41	100	8.4	341	2	Q819K3 BRAFL	Q819k3 brachiosteo
42	100	8.4	401	2	Q08835 CERAE	Q08835 cercopithec
43	99.5	8.3	289	2	Q6GX36 MOUSE	Q6gx36 mus musculus
44	99.5	8.3	356	2	Q8AXL7 ONCMY	Q8axl7 oncorhynchu
45	99.5	8.3	359	1	HPLN3 MOUSE	Q80wm5 mus musculus

ALIGNMENTS

RESULT 1

Q9UKJ0 HUMAN
ID Q9UKJ0 HUMAN PRELIMINARY; PRT; 227 AA.
AC Q9UKJ0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE Activating receptor PILRBeta (Hypothetical protein DKFzp340079).
GN Name=DKFzp340079;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banyville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRBeta, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is paired with the truncated counterpart PILRBeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
TISSUE=restis;
RG The German CDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION:
CC O95870:BAT5; NbExp=1; IntAct=EBI-347958, EBI-348517;
CC EMBL; AP161081; AAD52965.1; -; mRNA.
CC EMBL; AL834336; CAH10711.1; -; mRNA.
DR IntAct; Q9UKJ0; -.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007171; F:transmembrane receptor protein tyrosine kin. . .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain; Receptor.
SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7BF09 CRC64;

Query Match 100.0%; Score 1192; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 4e-101;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGRPLLLLLLLLLQPPAFLOPCGSGSPSYLYGVTPKHLASMGSGSVEIPFSYPWE	60
DB	1	MGRPLLLLLLLLLQPPAFLOPCGSGSPSYLYGVTPKHLASMGSGSVEIPFSYPWE	60
QY	61	LAIVNVRISWRGHFGQSFYSTPPSIHKDYVNRLEFLNWTGQESGFLRISNLKEDQ	120

```
Db 61 LAIVPNVRISWRRGHFHQSGFSYSTRPSPSIHKDYVNRFLNWTQESGFLRISNLKEDQ 120
Qy 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTTTTWRPSSTTIAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTTTTWRPSSTTIAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVLTKVILGLLCLLLMWRRRKSGRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVLTKVILGLLCLLLMWRRRKSGRAPSSDF 227

RESULT 2
Q9UKJ1 HUMAN
ID Q9UKJ1 HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PILRBeta.";
RL J. Biol. Chem. 275:4467-4474(2000)
DR EMBL; AF161080; AAD2964.1; -; mRNA.
DR Ensembl; ENSG0000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; P:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADF7E80928B CRC64;

Query Match 80.4%; Score 958; DB 2; Length 303;
Best Local Similarity 80.8%; Pred. No. 1.8e-79;
Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRRGHFHQSGFSYSTRPSPSIHKDYVNRFLNWTQESGFLRISNLKEDQ 120
Db 61 LATAPDVRIISWRRGHFHQSGFSYSTRPSPSIHKDYVNRFLNWTQESGFLRISNLKEDQ 120
Qy 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTT-----TTWRPSSTTIAGLRV 172
Db 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTTTQRPSSMTTWRLSSTTTTIGLRV 180
Qy 173 TESKGHSSWHLSDTAIRVALAVLTKVILGLLCLLLMWRRRKSGR 221
Db 181 TGKRRSDSWHISLETAVGVAVTVLGIMILGLICLLR--WRRKGGQ 227

RESULT 3
Q8NH11 HUMAN
ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH11
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OS PILRA protein.
DB Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017812; AAH1781.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;

Query Match 62.4%; Score 744; DB 2; Length 226;
Best Local Similarity 86.4%; Pred. No. 5.6e-60;
Matches 140; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRRGHFHQSGFSYSTRPSPSIHKDYVNRFLNWTQESGFLRISNLKEDQ 120
Db 61 LATAPDVRIISWRRGHFHQSGFSYSTRPSPSIHKDYVNRFLNWTQESGFLRISNLKEDQ 120
Qy 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTTTTWRPS 162
Db 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTTTTWRPS 162

RESULT 4
Q8BYA6 MOUSE
ID Q8BYA6 MOUSE PRELIMINARY; PRT; 299 AA.
AC Q8BYA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630007f20 product:weakly similar to INHIBITORY
DE RECEPTOR PILRALPHA.
GN Name=Pilra; Synonyms=AV021745;
OS Mus musculus (Mouse).
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 23.6581 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-6
Perfect score: 1192
Sequence: 1 MGRPLLLPLLLLPAPFLQ.....CLLLWRRRKGSRAPSSDF 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/PCUS-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1192	100.0	227	2	US-09-869-388-6
2	1163.5	97.6	226	2	US-09-869-388-10
3	1069	89.7	238	2	US-09-149-478-485
4	958	80.4	303	2	US-08-985-950-2
5	958	80.4	303	2	US-09-546-049-2
6	958	80.4	303	2	US-09-869-388-2
7	744	62.4	230	2	US-09-869-388-4
8	742.5	62.3	175	2	US-09-869-388-8
9	532	44.6	101	2	US-09-149-478-754
10	223	18.7	99	2	US-08-985-950-4
11	223	18.7	99	2	US-09-546-049-4
12	114	9.6	143	1	US-08-345-321-8
13	112	9.4	352	2	US-09-203-958A-2
14	110.5	9.3	310	2	US-09-079-029-11
15	107.5	9.0	440	2	US-09-866-028-61
16	107.5	9.0	440	2	US-09-944-457-61
17	107.5	9.0	440	2	US-09-945-584-61
18	107.5	9.0	440	2	US-09-944-944-61
19	107.5	9.0	440	2	US-09-945-587-61
20	107.5	9.0	442	2	US-09-778-510-20
21	107.5	9.0	442	2	US-09-930-803-1
22	107	9.0	476	2	US-09-291-299A-3
23	106.5	8.9	423	2	US-09-778-510-22
24	106	8.9	354	2	US-09-393-627B-28
25	105.5	8.9	244	2	US-08-918-148-79
26	105.5	8.9	244	2	US-09-138-091A-77
27	101.5	8.5	284	2	US-08-564-164A-2

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28 101.5 8.5 417 2 US-09-949-016-6729 Sequence 6729, Ap
29 101.5 8.5 456 2 US-09-949-016-7564 Sequence 7564, Ap
30 101 8.5 280 2 US-09-260-527-1 Sequence 1, Appli
31 100.5 8.4 479 2 US-09-723-368-2 Sequence 2, Appli
32 100.5 8.4 479 2 US-09-949-016-6278 Sequence 6278, Ap
33 100.5 8.4 522 2 US-09-949-016-7563 Sequence 7563, Ap
34 99.5 8.3 225 2 US-09-456-090A-66 Sequence 66, Appli
35 99.5 8.3 225 2 US-09-453-234-66 Sequence 66, Appli
36 99.5 8.3 312 2 US-09-079-029-10 Sequence 10, Appli
37 99 8.3 265 1 US-08-403-853-16 Sequence 16, Appli
38 99 8.3 355 2 US-08-875-811-57 Sequence 57, Appli
39 98.5 8.3 421 2 US-08-759-628-5 Sequence 5, Appli
40 98.5 8.3 622 1 US-08-356-785-16 Sequence 16, Appli
41 98 8.2 159 1 US-08-653-402B-2 Sequence 2, Appli
42 98 8.2 225 2 US-09-456-090A-70 Sequence 70, Appli
43 98 8.2 225 2 US-09-453-234-70 Sequence 70, Appli
44 98 8.2 360 2 US-09-907-794A-213 Sequence 213, App
45 98 8.2 360 2 US-09-905-125A-213 Sequence 213, App

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ALIGNMENTS

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RESULT 1
US-09-869-388-6
; Sequence 6, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 6
; LENGTH: 227
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-6

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Query Match 100.0%; Score 1192; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
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Qy 1 MGRPLLLPLLLLPAPFLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPSFYYPWE 60
Db 1 MGRPLLLPLLLLPAPFLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPSFYYPWE 60

Qy 61 LAIPNVIRISWRRGHFGQSFYSTRPPIHDKYVNRFLPLNWTGQSGFLRISNLRKEQ 120
Db 61 LAIPNVIRISWRRGHFGQSFYSTRPPIHDKYVNRFLPLNWTGQSGFLRISNLRKEQ 120

Qy 121 SYVFCRVELDTRRSRGRQQLQSIKTKLTITQAVTTTTTWRPSSSTTTIAGLRVTEKHS 180
Db 121 SYVFCRVELDTRRSRGRQQLQSIKTKLTITQAVTTTTTWRPSSSTTTIAGLRVTEKHS 180

Qy 181 SWHLSLDTAIRVALAVAVKTVILGLCLLLWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVAVKTVILGLCLLLWRRRKGSRAPSSDF 227

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RESULT 2
US-09-869-388-10
; Sequence 10, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel

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APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 10
LENGTH: 226
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-10

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Best Local Similarity 98.2%; Pred. No. 1.3e-111;
Matches 223; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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Db 61 LATAPDVRIISWRGHGHSQSYSTRPPSIHKDYVNRFLFNWTEGSGFLRISNLRKEDQ 120

Qy 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSRQQLQSIKTKLTITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180

Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLMWRRRKGSRAPSSDP 227
Db 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLMWRRRKGSRAPSSDF 226

RESULT 3
US-09-149-476-485
Sequence 485, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 166 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Total number of hits satisfying chosen parameters: 2443163

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1176.5	96.2	303	3	AAB07443 A human m
5	1173.5	96.0	303	8	ADP25129 PRO polyp
6	1057	86.4	206	7	AD95580 Human NOV
7	974	79.6	228	8	ADK98565 Human imm
8	830	67.9	1012	4	ABG00509 Novel hum
9	830	67.9	1012	4	ABG16869 Novel hum
10	830	67.9	1012	4	ABG02851 Novel hum
11	830	67.9	1012	4	ABG21403 Novel hum
12	816	66.7	175	3	AAB07446 A human m
13	765	62.6	226	2	AAW80407 A secrete
14	765	62.6	226	5	ABP61825 Human pol
15	759	62.1	226	2	AAV08015 Human LSP
16	759	62.1	226	3	AAB07447 A human m
17	745	60.9	238	5	ABG95345 Human nov
18	745	60.9	238	6	ABO34539 Region of
19	745	60.9	238	7	ADI23200 Novel hum
20	745	60.9	238	8	ADH74202 Human sec
21	744	60.8	227	3	AAB07445 A human m
22	744	60.8	227	6	ABU89824 TNF-recep
23	744	60.8	291	2	AAW63682 Human sec
24	744	60.8	326	4	ABB12010 Human sec

RESULT 1
AAB07444
ID AAB07444 standard; protein; 230 AA.
XX
AC AAB07444;
XX
DT 20-OCT-2000 (first entry)
XX
DB A human monocyte-derived protein FDF03Deltatm.
XX
KW Human; monocyte-derived protein; FDF03; FDF03Deltatm; FDF03-S1;
FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
tissue rejection; inflammation; infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide i.17
FT Protein /note= "signal peptide"
FT Protein 18..230
FT Protein /note= "mature protein"
XX
PN WO2000040721-A1.
XX
PD 13-JUL-2000.
XX
PF 29-DEC-1999; 99WO-US0300004.
XX
PR 31-DEC-1998; 98US-00223919.
PR 31-DEC-1998; 98US-00224604.
XX
PA (SCHE) SCHERING CORP.
XX
PI Bates E, Fournier N, Chaulus L, Garrone P;
XX
DR WPI; 2000-465994/40.
DR N-PSDB; AAA58815.
XX
PT Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
PT diseases associated with changes in monocyte numbers, e.g. bacterial or
PT viral infections.
XX
PS Claim 1; Page 34-35; 45pp; English.
XX
CC The present sequence represents a human monocyte-derived protein. The
CC specification describes monocyte-derived proteins FDF03, FDF03Deltatm,
CC FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the

ALIGNMENTS

25	731	59.8	227	3	AAV87230	Aay97230 Human sig
26	517	42.3	101	2	AAW75053	Aaw75053 Fragment
27	517	42.3	101	5	ABG95614	Abg95614 Human nov
28	517	42.3	101	6	ABO34808	Abo34808 Fragment
29	517	42.3	101	7	ADI23469	Adi23469 Novel hum
30	517	42.3	101	8	ADH74471	Adh74471 Human sec
31	354	28.9	224	5	ABH72387	Abh72387 Murine pr
32	348.5	28.5	212	7	ADE59537	Ade59537 Rat prote
33	222	18.2	99	2	AAW62773	Aaw62773 Partial m
34	120	9.8	577	4	AAH19872	Aah19872 Activatin
35	116.5	9.5	253	6	ABU97144	Abu97144 Recombina
36	115.5	9.4	247	6	ABU97118	Abu97118 Recombina
37	115.5	9.4	1700	5	ABO50444	Abb05044 Human NOV
38	115.5	9.4	1700	8	ADH71518	Adh71518 Human pro
39	115.5	9.4	1700	8	ADH71522	Adh71522 Human pro
40	115.5	9.4	1700	8	ADH71502	Adh71502 Human pro
41	115.5	9.4	1700	8	ADH71520	Adh71520 Human pro
42	115.5	9.4	1700	8	ADH71516	Adh71516 Human pro
43	114.5	9.4	252	6	ABU97128	Abu97128 Recombina
44	114.5	9.4	253	6	ABU97134	Abu97134 Recombina
45	114.5	9.4	253	8	ADS09256	Ads09256 Human C-M

CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocytic-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocytic hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX Sequence 230 AA;

Query Match 100.0%; Score 1223; DB 3; Length 230;
 Best Local Similarity 100.0%; Pred. No. 5.1e-97;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Qy 61 LATAPDVRIISWRGHFGQSFYSTRPPIHDKYVNLPLNWTGKSGFLRISNLQKDD 120
 Db 61 LATAPDVRIISWRGHFGQSFYSTRPPIHDKYVNLPLNWTGKSGFLRISNLQKDD 120
 Qy 121 SVYFCRVELDRSSGRQWQSIETGKLSITQOQRTKATTPAREPFPQNTPEYINRNEG 180
 Db 121 SVYFCRVELDRSSGRQWQSIETGKLSITQOQRTKATTPAREPFPQNTPEYINRNEG 180
 Qy 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSVLKA 230
 Db 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSVLKA 230

RESULT 2

ID ADE95578
 AD ADE95578 standard; protein; 230 AA.

AC ADE95578;

DT 12-FEB-2004 (first entry)

DE Human NOVX18a protein.

KW NOVX protein; biochemical stimulation; physiological stimulation;
 KW cardiant; antiatherosclerotic; hypotensive; cytostatic; anorectic;
 KW antiinflammatory; antiarthritic; antidiabetic; nephrotropic; dermatological;
 KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
 KW neurotropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
 KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
 KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
 KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
 KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
 KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
 KW depression; allergy; fertility disorder; NOVX18a.

OS Homo sapiens.

PN WO2003050245-A2.

PD 19-JUN-2003.

PF 03-DEC-2002; 2002WO-US038594.

XX 05-DEC-2001; 2001US-0336600P.

PR 07-DEC-2001; 2001US-0338285P.

PR 12-DEC-2001; 2001US-0341346P.

PR 17-DEC-2001; 2001US-0341477P.

PR 17-DEC-2001; 2001US-0341540P.

PR 20-DEC-2001; 2001US-0342592P.

PR 27-DEC-2001; 2001US-0344297P.

PR 31-DEC-2001; 2001US-0344903P.

PR 17-APR-2002; 2002US-0373288P.

PR 15-MAY-2002; 2002US-0380981P.
 PR 17-MAY-2002; 2002US-0381495P.
 PR 28-MAY-2002; 2002US-038334P.
 PR 28-MAY-2002; 2002US-0383744P.
 PR 29-MAY-2002; 2002US-0383829P.
 PR 29-MAY-2002; 2002US-0384024P.
 PR 07-AUG-2002; 2002US-0401788P.
 PR 26-AUG-2002; 2002US-0406353P.
 PR 31-OCT-2002; 2002US-0401788.
 PR 02-DEC-2002; 2002US-0406353.
 XX

PA (CURA-) CURAGEN CORP.

XX Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
 PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
 PI Jeffers MB, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
 PI Patturajan M, Feyman JA, Rastelli L, Rieger DK, Shenoy SG;
 PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
 XX WPI: 2003-513974/48.
 DR N-PSDB; ADE95577.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

PS Claim 2; SEQ ID NO 110; 211pp; English.

XX This invention relates to novel NOVX proteins, and the DNA sequence which
 CC encode them, having properties related to stimulation of biochemical or
 CC physiological responses in a cell, a tissue, an organ or an organism.
 CC Compounds which modulate the proteins of the invention may have cardiant,
 CC antiatherosclerotic, hypotensive, cytostatic, anorectic, antineumatic,
 CC antiarthritic, antidiabetic, nephrotropic, dermatological,
 CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
 CC neurotropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
 CC antidepressant, antiallergic or gynaecological activities. The DNA
 CC sequences of the invention may be useful for gene therapy whilst the
 CC protein sequences may allow the development of a vaccine. The protein is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease. The invention may be useful in
 CC diagnosing, treating or preventing NOVX-associated disorders, for example
 CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
 CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
 CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
 CC fertility disorders. The nucleic acids may further be used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine, and pharmacogenomics. The present sequence is the amino acid
 CC sequence of the human NOVX18a protein of the invention.

XX Sequence 230 AA;

Query Match 99.6%; Score 1218; DB 7; Length 230;
 Best Local Similarity 99.6%; Pred. No. 1.4e-96;
 Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Qy 61 LATAPDVRIISWRGHFGQSFYSTRPPIHDKYVNLPLNWTGKSGFLRISNLQKDD 120
 Db 61 LATAPDVRIISWRGHFGQSFYSTRPPIHDKYVNLPLNWTGKSGFLRISNLQKDD 120
 Qy 121 SVYFCRVELDRSSGRQWQSIETGKLSITQOQRTKATTPAREPFPQNTPEYINRNEG 180
 Db 121 SVYFCRVELDRSSGRQWQSIETGKLSITQOQRTKATTPAREPFPQNTPEYINRNEG 180
 Qy 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSVLKA 230
 Db 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSVLKA 230

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:08 ; Search time 16.0465 Seconds
(without alignments)
1379.107 Million cell updates/sec

Title: US-10-780-043-4
Perfect score: 1223
Sequence: 1 MGRPLLLPLLLPAPLQ.....PSHRPLKSPQNETLYSLVLA 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	109	8.9	sialoadhesin - mou
2	104.5	8.5	Ig Y heavy chain (
3	101	8.3	Ig heavy chain V r
4	100.5	8.2	rearranged T-cell
5	99	8.1	Ig lambda chain -
6	98	8.0	receptor tyrosine
7	97.5	8.0	colon carcinoma-as
8	97.5	8.0	probable neural ce
9	97	7.9	Ig gamma-2 chain -
10	97	7.9	VpreB protein prec
11	96.5	7.9	Ig lambda chain V-
12	96.5	7.9	elastic titin - hu
13	96	7.8	VpreB protein prec
14	95.5	7.8	Ig heavy chain pre
15	95.5	7.8	Ig light chain V r
16	94.5	7.7	protein-tyrosine k
17	94	7.7	T-cell receptor de
18	93.5	7.6	Ig lambda chain pr
19	93.5	7.6	Ig lambda chain pr
20	93.5	7.6	Ig heavy chain V r
21	93	7.6	MHC class II I-A-a
22	93	7.6	rearranged T-cell
23	93	7.6	T-cell receptor de
24	93	7.6	antigen BGM1 precu
25	93	7.6	m33-B isoform - mo
26	93	7.6	titin, cardiac mus
27	93	7.6	Ig lambda chain V-
28	92.5	7.6	Ig lambda chain V-
29	92.5	7.6	Ig lambda chain V-

30	92	7.5	125	2	A31493	Ig light chain pre
31	91.5	7.5	137	2	S36311	T-cell receptor de
32	91.5	7.5	233	2	S25747	Ig lambda chain -
33	91	7.4	112	2	S31515	Ig lambda chain V
34	91	7.4	113	1	L1CHV	Ig lambda chain pr
35	91	7.4	145	2	S36299	T-cell receptor de
36	90.5	7.4	118	2	S04519	Ig lambda chain pr
37	90.5	7.4	235	2	S14675	Ig lambda chain -
38	90	7.4	110	2	S51149	antibody light cha
39	90	7.4	112	2	S44105	Ig lambda chain V-
40	90	7.4	135	2	S36298	T-cell receptor de
41	90	7.4	143	2	S36300	T-cell receptor de
42	90	7.4	149	2	S36317	T-cell receptor de
43	90	7.4	880	1	JC4166	protein-tyrosine k
44	90	7.4	1333	2	I78875	receptor tyrosine
45	90	7.4	2124	2	A28452	proteoglycan core

ALIGNMENTS

RESULT 1

S50065
sialoadhesin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S50065
R:Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; M1
EMBO J. 13, 4490-4503, 1994
A:Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells
A:Reference number: S50065; MUID:95009950; PMID:7925291
A:Accession: S50065
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1694 <CRO>
A:Cross-references: UNIPROT:Q62230; UNIPARC:UPI000028874; EMBL:Z36293; NID:G557253; PFI

Query Match 8.9%; . Score 109; DB 2; Length 1694;
Best Local Similarity 22.5%; Pred. No. 0.86;
Matches 38; Conservative 30; Mismatches 77; Indels 24; Gaps 6;

QY	33	YGVTPKHLASMGSGVEIPFSPFYYPWELATAPDVRI	SWRRGHFHQS-----FYSTRP 86
Db	21	MGVSPKVNQVGLSGCLLIPCFISYPDPVNSNGITAIW	-----YYDSKGRQVWIHSQDP 76
QY	87	PSIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDSVY	FCRVELDRSSGRQWQSTEGTK 146
Db	77	KLVDKRFGRRAELMGMDHKVCNLLKDKPEDSGTYN	FRPEI-----SDSNRLDVKGIT 132
QY	147	LSITQGOQRTKATTP--AREPFQ---NTEEPY----	ENRVEGQNTDP 185
Db	133	VTVTTPSPPTTITPEELREGMERNFNCSTPYLCLQEK	QVSLQWRGQDP 181

RESULT 2

B46529
Ig Y heavy chain (7.8S) - duck
N:Alternate names: Ig gamma chain (7.8S)
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A:Title: Structural relationship between the two IGY of the duck, Anas platyrhynchos: m
A:Reference number: A46529; MUID:93017865; PMID:1401901
A:Accession: B46529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAG>
A:Cross-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:G62442; PIDN:CAA46322.1; PFI
A:Experimental source: spleen
A>Note: sequence extracted from NCBI backbone (NCBIP:116127)
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin
F;37-120/Domain: immunoglobulin homology <IMM>

Query Match 8.5%; Score 104.5; DB 2; Length 572;
Best Local Similarity 22.2%; Pred. No. 0.51;
Matches 49; Conservative 36; Mismatches 91; Indels 45; Gaps 10;

Qy 5 LLLPPLLPPAPFLQPSGSGSYLYGVTPQKHLASMGSGSVEI-----PFSPYY 57
Db 12 LLLAAVPLRAAATLDESG-----GLVSP-----GGSLTLVCKSGGFTFSYG 55

Qy 58 PWELATAPDVIRISWRRG--HFHGQSFTSRPPSIHKDYVNLFLNWTGQKSGFLRISNL 115
Db 56 VSWVRQAPGKLEWVAGITDSGGTYTA--PAVK---GRFTISRNNGQSTATLQNSL 108

Qy 116 QKQDOSVYFCRVEL--DTRSGRQMOISIEGTLKLSITQOQRTKATTPAREPFQNT--EEP 172
Db 109 KASDTATYCYKAGYAGIRSIDILWG--HGTVAVSSGSTAPSVFPISSCCGTOQQP 166

Qy 173 YENIRNEGQNTDPKLNPKDDGIVYASLASLSSTSPRAPPSH 213
Db 167 VVGCLATGYIPG-----VTFSMGASGATSVTPETH 199

RESULT 3
E27889
Ig heavy chain V region (H18-S415) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: E27889
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: E27889
A;Molecule type: DNA
A;Residues: 1-118 <CAT>
A;Cross-references: UNIPARC:UPI0000176B69
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 8.3%; Score 101; DB 2; Length 118;
Best Local Similarity 24.8%; Pred. No. 0.14;
Matches 33; Conservative 25; Mismatches 35; Indels 40; Gaps 7;

Qy 34 GVTQPKHLASMGSGVE-----IPFSFYFPELATAPDVIRISWRRGHFHGQSFYSTRP 86
Db 10 GLVXP-----GGSLKLSCAASGITFSDYVYWRQTPDKLEW-----VATIT 52

Qy 87 PSI----HKQVYNRLFLNWTGQKSGFLRISNLQKQDOSVYFCRVELDTRSS-----GRQ 137
Db 53 DDINVTYVSDVSGKFTISRDNAXNLYQLSLKSEDTAMYC-----TRGSYYVDYGM 107

Qy 138 QMQSIEGTLKLSIT 150
Db 108 YWG--QGTSTVTS 118

RESULT 4
I46626
rearranged T-cell receptor delta-chain/ Vdelta1.4-Ddelta3-Jdelta1 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C;Accession: I46626
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A;Reference number: I46623; MUID:95363165; PMID:7636249
A;Accession: I46626

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-151 <YAN>
A;Cross-references: UNIPARC:UPI000011B2A5; GB:D49567; NID:G1041136; PIDN:BAA08511.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 8.2%; Score 100.5; DB 2; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.2;
Matches 39; Conservative 17; Mismatches 50; Indels 35; Gaps 4;

Qy 6 LLLPPLLPPAPFLQPSGSGSYLYGVTPQKHLASMGSGSVEIPFSFYFPELATAP 65
Db 3 LSSLLMLFLTSVP-----SGSGVAQKVTDQPV--VSRQVGEAVTLNCRVETSMNEYTI- 54

Qy 66 DVIRISWRRGHFHGQSFYSTSRPPSIHKDYV-----NRLPLNWTGQKSGFLRIS 113
Db 55 -----FWYKQPPSGEMTFLIYQYSASRNAKDGRYFINFQAKQSLSTIS 99

Qy 114 NLQKQDOSVYFCRVELDTRSS 134
Db 100 ALQLQDSATYFCALWVVTMS 120

RESULT 5
S25758
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25758
R;Combrinato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25758
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: UNIPARC:UPI0000115F06; EMBL:X57823; NID:q33745; PIDN:CAA40960.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match 8.1%; Score 99; DB 2; Length 235;
Best Local Similarity 28.4%; Pred. No. 0.48;
Matches 44; Conservative 20; Mismatches 59; Indels 32; Gaps 8;

Qy 26 GSGSYLYGVTPQKHLASMGSGSVEIPFSFYFPELATAPDVIRISWRRGHFHGQSFYSTR 85
Db 14 GTGSAQSAQTQAPASVSGSPQSITISCT-----GSSSDV-----GGYNYVSWYQQH 60

Qy 86 PPSIHK-----DYVNL--FLNWTGQKSG---FLRISNLQKQDOSVYFCRVELDTRSSGR 136
Db 61 PGKAPKLMYDVNRPNSGVNRFSGSKSGNTASLTISGLQPEADYYC-----TSKTSS 115

Qy 137 QMQSIEGTLKLSITQOQRTKATT---PAREPFQ 167
Db 116 SFYVFGTGKVSUL-GQPKANPTVTLFPSPSEELQ 149

RESULT 6
I38912
receptor tyrosine kinase - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
C;Accession: I38912
R;Crosier, K.E.; Hall, L.R.; Lewis, P.M.; Morris, C.M.; Wood, C.R.; Morris, J.C.; Crosie
Growth Factors 11, 137-144, 1994
A;Title: Isolation and characterization of the human DPK receptor tyrosine kinase.
A;Reference number: I38912; MUID:95161080; PMID:7857658
A;Accession: I38912
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 99.2506 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-4
Perfect score: 1223
Sequence: 1 MGRPLLLPLLLPPAPFLQ.....PSHRPLKSPQNETLYSLVLA 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173.5	96.0	303	Q9UKJ1_HUMAN	Q9ukj1 homo sapien
2	1044	85.4	226	Q8NH11_HUMAN	Q8nh11 homo sapien
3	744	60.8	227	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
4	505.5	41.3	299	Q8BYA6_MOUSE	Q8bya6 mus musculus
5	126	10.3	633	Q5W434_BRARE	Q5w434 brachydanio
6	126	10.3	651	Q5W433_BRARE	Q5w433 brachydanio
7	113.5	9.3	1709	1 SN_HUMAN	Q9b222 homo sapien
8	111.5	9.1	233	Q8TBC9_HUMAN	Q8tbc9 homo sapien
9	109.5	9.0	386	Q58DE8_BOVIN	Q58de8 bos taurus
10	109	8.9	1694	1 SN_MOUSE	Q62230 mus musculus
11	109	8.9	1730	Q7YRQ7_PIG	Q7yrq7 sus scrofa
12	106	8.7	400	Q4T054_TETNG	Q4t054 tetraodon n
13	104	8.5	285	Q9JME9_MOUSE	Q9jme9 mus musculus
14	104	8.5	512	Q96DN8_HUMAN	Q96dn8 homo sapien
15	104	8.5	5635	Q5TYR7_HUMAN	Q5tyr7 homo sapien
16	104	8.5	5636	Q9GRW7_HUMAN	Q9grw7 homo sapien
17	103.5	8.5	302	Q4T853_TETNG	Q4t853 tetraodon n
18	102.5	8.4	149	Q63YF8_HUMAN	Q63yf8 homo sapien
19	102.5	8.4	271	Q9HBS0_HUMAN	Q9hbs0 homo sapien
20	102.5	8.4	551	1 SGL5_HUMAN	Q15389 homo sapien
21	102	8.3	236	Q6PIQ7_HUMAN	Q6piq7 homo sapien
22	102	8.3	325	Q501V7_BRARE	Q501v7 brachydanio
23	101	8.3	477	2 Q510J1_RAT	Q510j1 rattus norv
24	99.5	8.1	235	Q6P2J1_HUMAN	Q6p2j1 homo sapien
25	99.5	8.1	870	Q5L6U6_CHLAB	Q5l6u6 chlamydomophi
26	99.5	8.1	1150	Q8BS24_MOUSE	Q8bs24 mus musculus
27	98	8.0	394	Q6UXG0_HUMAN	Q6uxg0 homo sapien
28	98	8.0	3950	Q7YRF5_CANFA	Q7yrf5 canis famil
29	97.5	8.0	416	Q7M048_RAT	Q7m048 rattus norv
30	97.5	8.0	439	1 NF1C_MOUSE	Q70255 mus musculus
31	97.5	8.0	595	2 Q5W431_FUGRU	Q5w431 fugu rubrip

32	97.5	8.0	630	2 Q5W436_FUGRU	Q5w436 fugu rubrip
33	97.5	8.0	648	2 Q5W435_FUGRU	Q5w435 fugu rubrip
34	97.5	8.0	1209	2 P70232_MOUSE	P70232 mus musculus
35	97	7.9	142	1 VPRL1_MOUSE	P13372 mus musculus
36	97	7.9	142	2 Q5W1K4_MOUSE	Q5w1k4 mus musculus
37	97	7.9	142	2 Q545E0_MOUSE	Q545e0 m 13 days e
38	97	7.9	487	2 Q8ZVX0_HUMAN	Q8zvx0 homo sapien
39	96.5	7.9	235	2 Q8PUG0_HUMAN	Q8pju0 homo sapien
40	96.5	7.9	235	2 Q99M11_MOUSE	Q99m11 mus musculus
41	96.5	7.9	439	2 Q70188_RAT	Q70188 rattus norv
42	96.5	7.9	479	2 Q7TMK4_MOUSE	Q7tmk4 mus musculus
43	96.5	7.9	7962	2 Q10465_HUMAN	Q10465 homo sapien
44	96.5	7.9	34350	2 Q8WZ42_HUMAN	Q8wz42 homo sapien
45	96	7.8	226	1 CD79A_HUMAN	P11912 homo sapien

ALIGNMENTS

RESULT 1

Q9UKJ1_HUMAN	PRELIMINARY;	PRT;	303 AA.
ID	Q9UKJ1		
AC	Q9UKJ1		
DT	01-MAY-2000	(TrEMBLrel. 13, Created)	
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Inhibitory receptor PILRALpha.		
GN	Name=PILRA;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
EX	MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;		
RA	Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;		
RT	"PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-		
RT	bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is		
RT	paired with the truncated counterpart PILRBeta.";		
RL	J. Biol. Chem. 275:4467-4474(2000).		
DR	EMBL; AF161080; AAS2964.1; -; mRNA.		
DR	Ensembl; ENSG00000085514; Homo sapiens.		
DR	HGNC; HGNC:20396; PILRA.		
DR	GO; GO:0005887; C:integral to plasma membrane; ISS.		
DR	GO; GO:0005515; P:protein binding; ISS.		
DR	GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; ISS.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	SMART; SM00409; IG; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Immunoglobulin domain; Receptor.		
SQ	SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;		
Query Match	96.0%; Score 1173.5; DB 2; Length 303;		
Best Local Similarity	75.6%; Pred. No. 7.7e-91;		
Matches 229; Conservative	1; Mismatches 0; Indels 73; Gaps 1;		
QY	1	MGRPLLLPLLLPPAPFLQSGSGSGSYLYGYVTPQKLSASMGSGSVEIPFSFYYPWE	60
Db	1	MGRPLLLPLLLPPAPFLQSGSGSGSYLYGYVTPQKLSASMGSGSVEIPFSFYYPWE	60
QY	61	LATAPDVRLSRGRGHFGHQSFSYSTRPPSHKHQDVNRLFLNWTGQKSGFLRISNLOKQDQ	120
Db	61	LATAPDVRLSRGRGHFGHQSFSYSTRPPSHKHQDVNRLFLNWTGQKSGFLRISNLOKQDQ	120
QY	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQ-----	151
Db	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSMTTWTWRLSSITTTTGLRV	180
QY	152	-----	167
Db	181	TGKRKSDSWHISLETAVGVAVTVLGMILGLICLLRWRRKGGQRTKATTPAREPQ	240

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QY 168 NTEPEYINIRNEGQNTDPKLNPKDDGIYVYASLALSSSTSPRAPPSHRPLKSPQNETLYSV 227
DB 241 NTEPEYINIRNEGQNTDPKLNPKDDGIYVYASLALSSSTSPKAPPSSHRPLKSPQNETLYSV 300
QY 228 LKA 230
DB 301 LKA 303

RESULT 2
Q8NH11 HUMAN
ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH11;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PILRA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzanski M.I., Skalska U., Smallos D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017812; AAH17812.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 5398181797733A30 CRC64;

Query Match 85.4%; Score 1044; DB 2; Length 226;
Best Local Similarity 90.7%; Pred. No. 4.6e-80;
Matches 196; Conservative 6; Mismatches 10; Indels 4; Gaps 1;

QY 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPKHLASMGGSVEIPFSFYFWE 60
DB 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPKHLASMGGSVEIPFSFYFWE 60
QY 61 LATAPDVIRISWRRGHFGQSFYSTPRPSIHKDYVNRFLNWTGQKSGFLRISNLKQDQ 120
DB 61 LATAPDVIRISWRRGHFGQSFYSTPRPSIHKDYVNRFLNWTGQKSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGOORTKATTPAREPFTPEYINIRNEG 180

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DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGOORTKATTPAREPFTPEYINIRNEG 180
QY 181 QNTDPKLNPKDDGIYVYASLALSSSTSPRAPPSHRPL 216
DB 181 QNTDPKLNPK- ---LHLTOSTQSPSPQEPERDPV 212

RESULT 3
Q9UKJ0 HUMAN
ID Q9UKJ0 HUMAN PRELIMINARY; PRT; 227 AA.
AC Q9UKJ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Activating receptor PtiRbeta (Hypothetical protein DKFZp434O079).
GN Name=DKFZp434O079;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Barville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PtiRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PtiRbeta."
RL J. Biol. Chem. 275:4467-4474 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- INTERACTION:
CC O95870:BAT5; NBEexp=1; IntAct=EBI-347958, EBI-348517;
DR EMBL; AF161081; AAD52965.1; -; mRNA.
DR EMBL; AL834336; CAH10711.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain; Receptor.
SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;

Query Match 60.8%; Score 744; DB 2; Length 227;
Best Local Similarity 86.4%; Pred. No. 1.1e-54;
Matches 140; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

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DB 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPKHLASMGGSVEIPFSFYFWE 60
QY 61 LATAPDVIRISWRRGHFGQSFYSTPRPSIHKDYVNRFLNWTGQKSGFLRISNLKQDQ 120
DB 61 LATAPDVIRISWRRGHFGQSFYSTPRPSIHKDYVNRFLNWTGQKSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGOORTKATTPA 162
DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGOORTKATTPA 162

RESULT 4
Q8BYA6 MOUSE
ID Q8BYA6 MOUSE PRELIMINARY; PRT; 299 AA.
AC Q8BYA6;

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 23.9707 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-4
Perfect score: 1223
Sequence: 1 MGRPILLPLPPLLPAPLQ.....PSHRPKSPQNETLYSVLKA 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/ECTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilea1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	230	2	US-09-869-388-4
2	1176.5	96.2	303	2	US-08-985-950-2
3	1176.5	96.2	303	2	US-09-546-049-2
4	1176.5	96.2	303	2	US-09-869-388-2
5	816	66.7	175	2	US-09-869-388-8
6	759	62.1	226	2	US-09-869-388-10
7	745	60.9	238	2	US-09-149-476-485
8	744	60.8	227	2	US-09-869-388-6
9	517	42.3	101	2	US-09-149-476-754
10	222	18.2	99	2	US-08-985-950-4
11	222	18.2	99	2	US-09-546-049-4
12	113.5	9.3	1709	2	US-09-949-016-10503
13	109.5	9.0	244	2	US-08-918-148-79
14	109.5	9.0	244	2	US-09-138-091A-77
15	102.5	8.4	551	2	US-08-896-537A-2
16	100	8.2	229	2	US-08-751-359-22
17	100	8.2	229	2	US-08-907-146-22
18	100	8.2	284	2	US-09-184-658-40
19	100	8.2	284	2	US-09-504-262D-40
20	98.5	8.1	159	1	US-08-653-402B-2
21	98	8.0	355	2	US-08-875-811-57
22	97.5	8.0	104	2	US-10-083-424-40
23	97	7.9	479	2	US-10-104-047-3871
24	96.5	7.9	143	1	US-08-345-321-8
25	96.5	7.9	1209	2	US-09-130-158A-2
26	96	7.8	226	2	US-09-311-784A-32
27	96	7.8	232	2	US-09-949-016-7589

28 96 7.8 232 2 US-09-949-016-7590 Sequence 7590, Ap
29 95.5 7.8 421 2 US-08-759-628-5 Sequence 5, Appl
30 95.5 7.8 553 1 US-08-661-052-16 Sequence 16, Appl
31 95.5 7.8 553 2 US-09-188-082-16 Sequence 16, Appl
32 95.5 7.8 553 2 US-09-364-088-16 Sequence 16, Appl
33 95.5 7.8 553 2 US-09-102-716-16 Sequence 16, Appl
34 95 7.8 360 2 US-09-907-794A-213 Sequence 213, App
35 95 7.8 360 2 US-09-905-125A-213 Sequence 213, App
36 95 7.8 360 2 US-09-902-775A-213 Sequence 213, App
37 95 7.8 360 2 US-09-906-700-213 Sequence 213, App
38 95 7.8 360 2 US-09-903-603A-213 Sequence 213, App
39 95 7.8 360 2 US-09-904-920A-213 Sequence 213, App
40 95 7.8 360 2 US-09-909-064-213 Sequence 213, App
41 95 7.8 360 2 US-09-905-381A-213 Sequence 213, App
42 95 7.8 360 2 US-09-906-618-213 Sequence 213, App
43 95 7.8 360 2 US-09-906-646-213 Sequence 213, App
44 95 7.8 360 2 US-09-904-462-213 Sequence 213, App
45 95 7.8 360 2 US-09-902-736A-213 Sequence 213, App

ALIGNMENTS

RESULT 1
US-09-869-388-4
; Sequence 4, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METH
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IEM PC compatible
; SEQ ID NO 4
; LENGTH: 230
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-4

Query Match 100.0%; Score 1223; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 3e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRPILLPLPPLLPAPLQPSGSGSYLYGVTPKHLASMGSGSVIIPFSFYYPWE 60
DB 1 MGRPILLPLPPLLPAPLQPSGSGSYLYGVTPKHLASMGSGSVIIPFSFYYPWE 60
QY 61 LATAPDVRISWRGRGHFGQSFYSTPPSIHKDYVNRFLNWTGQSGFLRISNLQKQDQ 120
DB 61 LATAPDVRISWRGRGHFGQSFYSTPPSIHKDYVNRFLNWTGQSGFLRISNLQKQDQ 120
QY 121 SYVFCRVELDTRSSGRQMQSIEGFKLSITQOQRTKATTPAREPQNTPEYINRNEG 180
DB 121 SYVFCRVELDTRSSGRQMQSIEGFKLSITQOQRTKATTPAREPQNTPEYINRNEG 180
QY 181 QNTDPKLNPKDGIYVASLALSSSTSPRAPPSHRPLKSPQNETLYSVLKA 230
DB 181 QNTDPKLNPKDGIYVASLALSSSTSPRAPPSHRPLKSPQNETLYSVLKA 230

RESULT 2
US-08-985-950-2
; Sequence 2, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22

;;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-985-950-2

Query Match 96.2%; Score 1176.5; DB 2; Length 303;
Best Local Similarity 75.9%; Pred. No. 1.4e-105;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

QY 1 MGRLLPLPLPAPLQSGSGPSVLYGVTPKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRLLPLPLPAPLQSGSGPSVLYGVTPKHLASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120
DB 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120

QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQ----- 151
DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTQRPSSMTTWRLLSSTTTTGLRV 180

QY 152 -----GQORTKATTAREPFQ 167
DB 181 TQKRRSDSWHISLETAVGVAVTVLGMILGLICLLRWRRKQKQRTKATTAREPFQ 240

QY 168 NTEPFYENIRNEGQNTDKLPKPDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 227
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QY 228 LKA 230
DB 301 LKA 303

RESULT 3

US-09-546-049-2
; Sequence 2, Application US/09546049
; Patent No. 6479638

;;
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosee Jan
; Meyaard, Linde
; Gorman, Daniel M.
; McClanahan, Terrill K.
; Zurawski, Sandra M.
; Zurawski, Gerard
; Lanier, Lewis L.
; Phillips Jr., Joseph H.
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; Related Reagents
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/546,049
; FILING DATE: 10-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-546-049-2

Query Match 96.2%; Score 1176.5; DB 2; Length 303;
Best Local Similarity 75.9%; Pred. No. 1.4e-105;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

QY 1 MGRLLPLPLPAPLQSGSGPSVLYGVTPKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRLLPLPLPAPLQSGSGPSVLYGVTPKHLASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120
DB 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120

QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQ----- 151
DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTQRPSSMTTWRLLSSTTTTGLRV 180

QY 152 -----GQORTKATTAREPFQ 167
DB 181 TQKRRSDSWHISLETAVGVAVTVLGMILGLICLLRWRRKQKQRTKATTAREPFQ 240

QY 168 NTEPFYENIRNEGQNTDKLPKPDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 227

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 78.2515 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-4
Perfect score: 1223
Sequence: 1 MGRPILLPLLLPPAFLO.....PSHRPLKSPQNETLYSVLKA 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications 'AA Main':
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	230	4	US-10-780-043-4 Sequence 4, Appli
2	1218	99.6	230	4	US-10-309-290-110 Sequence 110, Appl
3	1176.5	96.2	303	3	US-09-774-381-58 Sequence 58, Appl
4	1176.5	96.2	303	4	US-10-290-631-2 Sequence 2, Appli
5	1176.5	96.2	303	4	US-10-780-043-2 Sequence 2, Appli
6	1176.5	96.2	303	4	US-10-777-524-2 Sequence 2, Appli
7	1176.5	96.2	303	5	US-10-777-521-2 Sequence 2, Appli
8	1057	86.4	206	4	US-10-309-290-112 Sequence 112, App
9	830	67.9	1012	5	US-10-450-763-30868 Sequence 30868, A
10	830	67.9	1012	5	US-10-450-763-33210 Sequence 33210, A
11	830	67.9	1012	5	US-10-450-763-47228 Sequence 47228, A
12	830	67.9	1012	5	US-10-450-763-51762 Sequence 51762, A
13	816	66.7	175	4	US-10-780-043-8 Sequence 8, Appli
14	765	62.6	226	3	US-09-745-763-106 Sequence 106, App
15	759	62.1	226	3	US-09-774-381-44 Sequence 44, Appl
16	759	62.1	226	4	US-10-780-043-10 Sequence 10, Appl
17	745	60.9	238	3	US-09-809-391-485 Sequence 485, App
18	745	60.9	238	3	US-09-882-171-485 Sequence 485, App
19	745	60.9	238	4	US-10-164-861-485 Sequence 485, App
20	744	60.8	227	4	US-10-262-445-128 Sequence 128, App
21	744	60.8	227	4	US-10-780-043-6 Sequence 6, Appli
22	744	60.8	227	5	US-10-820-474A-7 Sequence 7, Appli
23	744	60.8	291	3	US-09-935-390A-21 Sequence 21, Appl
24	744	60.8	326	4	US-10-276-774-2380 Sequence 2380, Ap
25	517	42.3	101	3	US-09-809-391-754 Sequence 754, App
26	517	42.3	101	3	US-09-882-171-754 Sequence 754, App
27	517	42.3	101	4	US-10-164-861-754 Sequence 754, App

28	354	28.9	224	3	US-09-866-050A-711	Sequence 711, App
29	222	18.2	99	4	US-10-290-631-4	Sequence 4, Appli
30	222	18.2	99	4	US-10-777-521-4	Sequence 4, Appli
31	222	18.2	99	5	US-10-777-521-4	Sequence 4, Appli
32	120.5	9.9	124	5	US-10-788-625-92	Sequence 92, Appli
33	116.5	9.5	253	4	US-10-479-670-184	Sequence 184, App
34	115.5	9.4	247	4	US-10-479-670-158	Sequence 158, App
35	115.5	9.4	1700	3	US-09-863-776-24	Sequence 24, Appl
36	114.5	9.4	252	4	US-10-479-670-168	Sequence 168, App
37	114.5	9.4	253	4	US-10-479-670-174	Sequence 174, App
38	114.5	9.4	253	4	US-10-779-461-18	Sequence 18, Appl
39	113.5	9.3	1694	4	US-10-203-708-36	Sequence 36, Appl
40	113.5	9.3	1709	3	US-09-870-759-51	Sequence 51, Appl
41	113.5	9.3	1709	3	US-09-751-708A-51	Sequence 51, Appl
42	113.5	9.3	1709	3	US-09-863-776-58	Sequence 58, Appl
43	113.5	9.3	1709	3	US-09-863-776-60	Sequence 60, Appl
44	113.5	9.3	1709	4	US-10-203-708-35	Sequence 35, Appl
45	113.5	9.3	1709	4	US-10-408-765A-1562	Sequence 1562, Ap

ALIGNMENTS

RESULT 1

US-10-780-043-4
; Sequence 4, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METH
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/10780, 043
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/869,388
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 4
; LENGTH: 230
; TYPE: PRF
; ORGANISM: homo sapiens
US-10-780-043-4

Query Match	100.0%	Score	1223	DB	4	Length	230
Best Local Similarity	100.0%	Pred. No.	2.8e-100	Mismatches	0	Indels	0
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Qy	1	MGRPILLPLLLPPAFLOPSGSGSYLYGVTPKHLASMGSGVEIPFSFYYPWE	60				
Db	1	MGRPILLPLLLPPAFLOPSGSGSYLYGVTPKHLASMGSGVEIPFSFYYPWE	60				
Qy	61	LATADVIRSWRGHFGQSPYTPPSIHKDYVRLFLNWTGQSGFLRISNLKQDQ	120				
Db	61	LATADVIRSWRGHFGQSPYTPPSIHKDYVRLFLNWTGQSGFLRISNLKQDQ	120				
Qy	121	SVYFCRVELDTRSSGRQWQSTEGTKLSITQOQRTKATTPAREPQNTPEEYENIRNEG	180				
Db	121	SVYFCRVELDTRSSGRQWQSTEGTKLSITQOQRTKATTPAREPQNTPEEYENIRNEG	180				
Qy	181	QNTDKPLNPKDGIYVYASIALSSSTSPRPPSHRPLKSPQNETLYSVLKA	230				
Db	181	QNTDKPLNPKDGIYVYASIALSSSTSPRPPSHRPLKSPQNETLYSVLKA	230				

RESULT 2

US-10-309-290-110
; Sequence 110, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.

APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Chilikuru, Rajeev A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gould-Rothberg, Bonnie E.
APPLICANT: Guo, Xiaojia
APPLICANT: Jeffers, Michael E.
APPLICANT: Ji, Weizhen
APPLICANT: Li, Li
APPLICANT: Malyankar, Uriel M.
APPLICANT: Miller, Charles E.
APPLICANT: Murphey, Ryan
APPLICANT: Patturajan, Meera
APPLICANT: Payman, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Smithson, Glenda
APPLICANT: Starling, Gary
APPLICANT: Taupier, Raymond J.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,285
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/341,540
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,297
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/380,981
PRIOR FILING DATE: 2002-05-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 110
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-290-110

Query Match 99.6%; Score 1218; DB 4; Length 230;
Best Local Similarity 99.6%; Pred. No. 7.7e-100;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
Db 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60

Qy 61 LATAPDVRIWRGHHFQSGFSYSTRPSIHKDYVNRFLNWTBQKSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGHHFQSGFSYSTRPSIHKDYVNRFLNWTBQKSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDRSSGRQWQSIETGKLSITQGGQRTKATTPAREPFONTPEYENIRNEG 180

Db 121 SVYFCRVELDRSSGRQWQSIETGKLSITQGGQRTKATTPAREPFONTPEYENIRNEG 180

Qy 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPSHPKSPQNETLYSVLKA 230
Db 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPSHPKSPQNETLYSVLKA 230

RESULT 3
US-09-774-381-58
Sequence 58, Application US/09774381
Publication No. US20030082677A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: McCarthy, Sean A.
APPLICANT: Pan, Yang
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL EDIPF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
FILE REFERENCE: MNI-107CP2
CURRENT APPLICATION NUMBER: US/09/774,381
CURRENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 08/941,354
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/010,674
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/061,149
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/014,347
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 60/061,159
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/474,151
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 09/004,206
PRIOR FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/061,143
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/483,414
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 09/213,571
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,890
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapiens
US-09-774-381-58

Query Match 96.2%; Score 1176.5; DB 3; Length 303;
Best Local Similarity 75.9%; Pred. No. 5.3e-96;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

Qy 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
Db 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60

Qy 61 LATAPDVRIWRGHHFQSGFSYSTRPSIHKDYVNRFLNWTBQKSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGHHFQSGFSYSTRPSIHKDYVNRFLNWTBQKSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDRSSGRQWQSIETGKLSITQ----- 151
Db 121 SVYFCRVELDRSSGRQWQSIETGKLSITQVTTTQRPFSMTTWRLSSTTTTGLRV 180

Qy 152 ----- 167
Db 152 ----- 167

Qy 168 NTEBPENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPSHPKSPQNETLYSV 227

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:41:30 ; Search time 4.35831 Seconds
(without alignments)
376.418 Million cell updates/sec

Title: US-10-780-043-4

Perfect score: 1233

Sequence: 1 MGRPILLPLPPLPPLPFLQ.....PSHRPLKSPQNTLYSVLKA 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New.*

- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US03_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113.5	9.3	1649	US-10-995-561-974	Sequence 974, App
2	113.5	9.3	1694	US-11-135-855-36	Sequence 36, Appl
3	113.5	9.3	1709	US-10-995-561-973	Sequence 973, Appl
4	113.5	9.3	1709	US-11-135-855-35	Sequence 35, Appl
5	112.5	9.2	258	US-10-512-184-26	Sequence 26, Appl
6	112.5	9.2	327	US-10-512-184-62	Sequence 62, Appl
7	112.5	9.2	327	US-10-512-184-64	Sequence 64, Appl
8	112.5	9.2	328	US-10-512-184-63	Sequence 63, Appl
9	112.5	9.2	576	US-10-512-184-65	Sequence 65, Appl
10	112.5	9.2	625	US-10-512-184-47	Sequence 47, Appl
11	110.5	9.0	246	US-11-054-515-2077	Sequence 2077, App
12	110.5	9.0	246	US-11-054-515-2079	Sequence 2079, App
13	108.5	8.9	256	US-11-054-515-907	Sequence 907, App
14	106.5	8.7	250	US-10-512-184-27	Sequence 27, Appl
15	106	8.7	250	US-11-054-515-1319	Sequence 1319, App
16	106	8.7	258	US-11-054-515-1841	Sequence 1841, App
17	103	8.4	251	US-11-054-515-1827	Sequence 1827, App
18	102.5	8.4	251	US-11-054-515-3247	Sequence 3247, App
19	102.5	8.4	252	US-11-054-515-1021	Sequence 1021, App
20	102.5	8.4	551	US-11-000-463-346	Sequence 346, App
21	102	8.3	245	US-11-054-515-1864	Sequence 1864, App
22	102	8.3	247	US-11-054-515-1751	Sequence 1751, App
23	102	8.3	250	US-11-054-515-837	Sequence 837, App
24	102	8.3	250	US-11-054-515-867	Sequence 867, App
25	102	8.3	250	US-11-054-515-1313	Sequence 1313, App

26	101.5	8.3	252	7	US-11-054-515-1787	Sequence 1787, App
27	100.5	8.2	242	7	US-11-054-515-1884	Sequence 1884, App
28	100.5	8.2	249	7	US-11-054-515-540	Sequence 540, App
29	100.5	8.2	254	7	US-11-054-515-1525	Sequence 1525, App
30	100.5	8.2	256	7	US-11-054-515-2080	Sequence 2080, App
31	100	8.2	250	7	US-11-054-515-1561	Sequence 1561, App
32	100	8.2	251	7	US-11-054-515-1046	Sequence 1046, App
33	100	8.2	251	7	US-11-054-515-1052	Sequence 1052, App
34	100	8.2	251	7	US-11-054-515-1053	Sequence 1053, App
35	99.5	8.1	249	7	US-11-054-515-708	Sequence 708, App
36	99	8.1	247	7	US-11-054-515-1704	Sequence 1704, App
37	99	8.1	249	7	US-11-054-515-2065	Sequence 2065, App
38	99	8.1	250	7	US-11-054-515-868	Sequence 868, App
39	99	8.1	250	7	US-11-054-515-933	Sequence 933, App
40	99	8.1	250	7	US-11-054-515-942	Sequence 942, App
41	99	8.1	251	7	US-11-054-515-852	Sequence 852, App
42	99	8.1	251	7	US-11-054-515-879	Sequence 879, App
43	99	8.1	251	7	US-11-054-515-940	Sequence 940, App
44	99	8.1	251	7	US-11-054-515-1047	Sequence 1047, App
45	99	8.1	251	7	US-11-054-515-1064	Sequence 1064, App

ALIGNMENTS

RESULT 1

US-10-995-561-974
; Sequence 974, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 974
; LENGTH: 1649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-974

Query Match 9.3%; Score 113.5; DB 6; Length 1649;
Best Local Similarity 24.2%; Pred. No. 0.021;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;
QY 10 LPILLPPALPQSGTSGPSYLYGVTPQKLSASMGGSVEIPFSGFYYPWELATAPDVR1 69
DB 4 LPKLLLLASFFPAGQAS-----WGVSSPDQGVKGSCLLIPCFSPFADVEVPDGIYA 57
QY 70 SWRRGHFHGQS---FYSTRPPSIHKDYNNRL-FLNWTBQKSGFLIRISNLKQDOSVYPC 125
DB 58 IWYI-DYSGQRQVSHSADPKLVEARFRGRTEFMGNPEHRVCNLL-LKDLQPEDSSSYNF 115
QY 126 RVELTRSGRQOWSIEGTKLSITQGGQRTKATTPAREPFONTE-----EPY-----EN 175
DB 116 REFI-----SEVNRWSDVKGTLVTVTEPRVPTIASPV-ELLEGTVEYDFNCSTFYVCLQSQ 170
QY 176 INNEGQNTDP 185
DB 171 VRLQWQQDP 180

RESULT 2

US-11-135-855-36
; Sequence 36, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.

```

; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-36

Query Match          9.3%; Score 113.5; DB 7; Length 1694;
Best Local Similarity 24.2%; Pred. No. 0.021;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;

Qy 10 LPLLLLPAPLQPSGSGSYLYGVTPQKHLASMGSGVEIPFSPYYPWELATAPDVRI 69
Db 4 LPKLLLLASFPFAGQAS-----WGVSSPDQVQGVKSGCLLIPCFISFPADVVPDGITA 57

Qy 70 SWRGHFGQS---FYSTRPSPHDKYVNRLL-FLNWTGQKSGFLRISNLQKQDSVYFC 125
Db 58 IWYI-DYSGQRQVSHSADPKLVEARFRGRTEFMGNPHEHVCNLL-LKDLPEDSGSYNF 115

Qy 126 RVELDTRSSGRQWQSIQEGTKLSITQOQRTKATTPAREPFQNT-----EPY-----EN 175
Db 116 RFEI-----SEVNRWSDVKGTLVTVTEPRVPTIASPV-ELLEGTVDVDFNCSTPYVCLQEQ 170

Qy 176 IRNEGQNTDP 185
Db 171 VRLQWQGD 180

RESULT 3
US-10-995-561-973
; Sequence 973, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 973
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-973

Query Match          9.3%; Score 113.5; DB 6; Length 1709;
Best Local Similarity 24.2%; Pred. No. 0.022;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;

Qy 10 LPLLLLPAPLQPSGSGSYLYGVTPQKHLASMGSGVEIPFSPYYPWELATAPDVRI 69
Db 4 LPKLLLLASFPFAGQAS-----WGVSSPDQVQGVKSGCLLIPCFISFPADVVPDGITA 57

Qy 70 SWRGHFGQS---FYSTRPSPHDKYVNRLL-FLNWTGQKSGFLRISNLQKQDSVYFC 125
Db 58 IWYI-DYSGQRQVSHSADPKLVEARFRGRTEFMGNPHEHVCNLL-LKDLPEDSGSYNF 115
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Qy 126 RVELDTRSSGRQWQSIQEGTKLSITQOQRTKATTPAREPFQNT-----EPY-----EN 175
Db 116 RFEI-----SEVNRWSDVKGTLVTVTEPRVPTIASPV-ELLEGTVDVDFNCSTPYVCLQEQ 170

Qy 176 IRNEGQNTDP 185
Db 171 VRLQWQGD 180

RESULT 4
US-11-135-855-35
; Sequence 35, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-35

Query Match          9.3%; Score 113.5; DB 7; Length 1709;
Best Local Similarity 24.2%; Pred. No. 0.022;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;

Qy 10 LPLLLLPAPLQPSGSGSYLYGVTPQKHLASMGSGVEIPFSPYYPWELATAPDVRI 69
Db 4 LPKLLLLASFPFAGQAS-----WGVSSPDQVQGVKSGCLLIPCFISFPADVVPDGITA 57

Qy 70 SWRGHFGQS---FYSTRPSPHDKYVNRLL-FLNWTGQKSGFLRISNLQKQDSVYFC 125
Db 58 IWYI-DYSGQRQVSHSADPKLVEARFRGRTEFMGNPHEHVCNLL-LKDLPEDSGSYNF 115

Qy 126 RVELDTRSSGRQWQSIQEGTKLSITQOQRTKATTPAREPFQNT-----EPY-----EN 175
Db 116 RFEI-----SEVNRWSDVKGTLVTVTEPRVPTIASPV-ELLEGTVDVDFNCSTPYVCLQEQ 170

Qy 176 IRNEGQNTDP 185
Db 171 VRLQWQGD 180

RESULT 5
US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 258
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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 23, 2005, 20:18:33 ; Search time 126.054 Seconds
(without alignments)
1056.147 Million cell updates/sec

Title: US-10-780-043-2
Perfect score: 1591
Sequence: 1 MGRPLLLPLLLPLPPAPLQ.....PSHRLKSPQNETLYSLVLA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1591	100.0	303	2	Aaw62772 Human imm
2	1591	100.0	303	3	Aab07443 A human m
3	1588	99.8	303	8	Adp25129 PRO polyp
4	1176.5	73.9	230	3	Aab07444 A human m
5	1171.5	73.6	230	7	Adp95578 Human NOV
6	1010.5	63.5	206	7	Adp95580 Human NOV
7	973.5	61.2	226	2	Aay08015 Human LSP
8	973.5	61.2	226	3	Aab07447 A human m
9	967.5	60.8	226	5	Aaw80407 A secrete
10	967.5	60.8	226	5	Abp61825 Human pol
11	958	60.2	227	3	Aab07445 A human m
12	958	60.2	227	6	Abu89824 TNF-recep
13	958	60.2	291	2	Aaw63682 Human sec
14	958	60.2	326	4	Abb12010 Human sec
15	945	59.4	227	3	Aay87230 Human sig
16	934	58.7	238	5	Abg95345 Human nov
17	934	58.7	238	6	Abg34539 Region of
18	934	58.7	238	8	Adh74202 Human hum
19	927.5	58.3	228	8	Adk98565 Human imm
20	927.5	58.3	228	8	Adk98565 Human imm
21	821	51.6	175	3	Aab07446 A human m
22	808	50.8	1012	4	Abg00509 Novel hum
23	808	50.8	1012	4	Abg16869 Novel hum
24	808	50.8	1012	4	Abg02851 Novel hum

25	808	50.8	1012	4	ABG21403	Abg21403 Novel hum
26	517	32.5	101	2	AAW75053	AAW75053 Fragment
27	517	32.5	101	5	ABG95614	ABG95614 Human nov
28	517	32.5	101	6	ABO34808	ABO34808 Fragment
29	517	32.5	101	7	ADI23469	ADI23469 Novel hum
30	517	32.5	101	8	ADH74471	ADH74471 Human sec
31	411	25.8	224	5	ABE72387	ABE72387 Murine pr
32	405.5	25.5	212	7	ADE59537	ADE59537 Rat Prote
33	222	14.0	99	2	AAW62773	AAW62773 Partial m
34	148.5	9.3	305	4	AAU14284	AAU14284 Human nov
35	148.5	9.3	305	9	ABE11270	ABE11270 Human Kil
36	146.5	9.2	305	4	AAU14520	AAU14520 Human nov
37	146.5	9.2	305	4	ABE66271	ABE66271 Human TAN
38	146.5	9.2	305	5	AAU08796	AAU08796 Human leu
39	146.5	9.2	305	5	AAO19216	AAO19216 Human sec
40	146.5	9.2	305	8	ADS11833	ADS11833 Human the
41	146.5	9.2	305	8	ADS11832	ADS11832 Human the
42	146.5	9.2	305	8	ADS11831	ADS11831 Human the
43	146.5	9.2	305	8	ADS10561	ADS10561 Human the
44	145.5	9.1	305	8	ADH80838	ADH80838 Human pol
45	139	8.7	290	4	AAW74712	AAW74712 Human mem

ALIGNMENTS

RESULT 1
AAW62772
ID AAW62772 standard; protein; 303 AA.
XX
AC AAW62772;
XX

DT 23-SEP-1998 (first entry)
XX
DE Human immunoglobulin receptor designated FDF03.
XX

KW Human; type I transmembrane protein; immunoglobulin-like domain; FDF03;
KW activated monocyte; YEO1; KTE03; control; development; differentiation;
KW mammalian immune system; treatment; cancerous condition;
KW degenerative condition; autoimmune response; transplantation rejection;
KW graft versus host disease; inflammatory condition; detection; diagnosis;
KW drug screening.
XX
OS Homo sapiens.
XX
PN WO9824906-A2.
XX
PD 11-JUN-1998.

PF 05-DEC-1997; 97WO-US021101.
XX
PR 06-DEC-1996; 96US-0032252P.
PR 09-DEC-1996; 96US-00762187.
PR 16-DEC-1996; 96US-0033181P.
PR 21-MAR-1997; 97US-0041279P.
XX
(SCHE) SCHERING CORP.

PI Adema CJ, Meygaard L, Gorman DM, Mcclanahan TK, Zurawski SM;
PI Zurawski G, Lanier LL, Phillips JH;
XX
DR WPI; 1998-333325/29.
DR N-PSDB; AAW38987.
XX

PT New isolated activated monocyte cell gene(s) - used to develop products
PT for treating e.g. cancer, degenerative conditions, autoimmune responses,
PT transplant rejection or inflammatory conditions.
XX
PS Claim 1; Page 60-61; 104pp; English.

CC The present sequence represents a human protein, FDF03, which is a type I
CC transmembrane protein comprising an extracellular portion characterised
CC by immunoglobulin-like domains, indicating that the protein is a receptor

CC member of the immunoglobulin superfamily. The FDF03 gene is found in
 CC activated monocytes. The specification also describes other proteins
 CC encoded by activated monocytes, which are designated YE01 and KTE03. The
 CC genes function in controlling development, differentiation, and/or
 CC physiology of the mammalian immune system. The products can be used for
 CC treating abnormal proliferation, regeneration, degeneration or atrophy.
 CC They can be used for treating e.g. cancerous conditions, degenerative
 CC conditions, autoimmune responses, transplantation rejection, graft versus
 CC host disease, or inflammatory conditions. The products can also be used
 CC for detection, diagnosis and drug screening

XX SQ Sequence 303 AA;

Query Match 100.0%; Score 1591; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.7e-122;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPPAFLLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Db 1 MGRPLLLPLLLPPAFLLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Qy 61 LATAPDVRIISWRGHFHGQSPSYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Db 61 LATAPDVRIISWRGHFHGQSPSYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Qy 121 SVYFCRVELDTRSSGRQMQSIEGTKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 180
 Db 121 SVYFCRVELDTRSSGRQMQSIEGTKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 180
 Qy 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGLICLLRWRRRKQQTATTTPAREPFPQ 240
 Db 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGLICLLRWRRRKQQTATTTPAREPFPQ 240
 Qy 241 NTEPEYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPSHRPLKSPQNETLYSV 300
 Db 241 NTEPEYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPSHRPLKSPQNETLYSV 300
 Qy 301 LKA 303
 Db 301 LKA 303

RESULT 2

AA07443
 ID AAB07443 standard; protein; 303 AA.

XX AC AAB07443;

XX DT 20-OCT-2000 (first entry)

XX DE A human monocyte-derived protein FDF03.

XX KW Human, monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
 KW FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KW tissue rejection; inflammation; infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "signal peptide"
 FT Protein 20..303
 FT Protein /note= "mature protein"

XX WO2000040721-A1.

XX PD 13-JUL-2000.

XX PF 29-DEC-1999; 99WO-US030004.

XX PR 31-DEC-1998; 98US-00223919.

XX PR 31-DEC-1998; 98US-00224604.

XX

PA (SCHE) SCHERING CORP.

XX PI Bates E, Fournier N, Chaulus L, Garrone P;

XX WPI; 2000-465984/40.

DR N-PSDB; AAA58814.

XX PT Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
 PT diseases associated with changes in monocyte numbers, e.g. bacterial or
 PT viral infections.

XX PS Claim 1; Page 32-33; 45pp; English.

XX CC The present sequence represents a human monocyte-derived protein. The
 CC specification describes monocyte-derived proteins FDF03, FDF03DeltaTM,
 CC FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
 CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocyte-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocyte hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX SQ Sequence 303 AA;

Query Match 100.0%; Score 1591; DB 3; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.7e-122;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPPAFLLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Db 1 MGRPLLLPLLLPPAFLLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Qy 61 LATAPDVRIISWRGHFHGQSPSYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Db 61 LATAPDVRIISWRGHFHGQSPSYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Qy 121 SVYFCRVELDTRSSGRQMQSIEGTKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 180
 Db 121 SVYFCRVELDTRSSGRQMQSIEGTKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 180
 Qy 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGLICLLRWRRRKQQTATTTPAREPFPQ 240
 Db 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGLICLLRWRRRKQQTATTTPAREPFPQ 240
 Qy 241 NTEPEYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPSHRPLKSPQNETLYSV 300
 Db 241 NTEPEYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPSHRPLKSPQNETLYSV 300
 Qy 301 LKA 303
 Db 301 LKA 303

RESULT 3

ADP25129
 ID ADP25129 standard; protein; 303 AA.

XX AC ADP25129;

XX DT 18-NOV-2004 (first entry)

XX DE PRO polypeptide SEQ ID NO:2307.

XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antiproliferative; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX OS Unidentified.

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 31.5788 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-2

Perfect score: 1591

Sequence: 1 MGRPILLPLLLPPAFLLQ.....PSHRPLKSPQNETLYSLVLA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/PCUTS COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1591	100.0	303	2	US-08-985-950-2
2	1591	100.0	303	2	US-09-546-049-2
3	1591	100.0	303	2	US-09-869-388-2
4	1176.5	73.9	230	2	US-09-869-388-4
5	973.5	61.2	226	2	US-09-869-388-10
6	958	60.2	227	2	US-09-869-388-6
7	934	58.7	238	2	US-09-149-476-485
8	821	51.6	175	2	US-09-869-388-8
9	517	32.5	101	2	US-09-149-476-754
10	222	14.0	99	2	US-08-985-950-4
11	222	14.0	99	2	US-09-546-049-4
12	130.5	8.2	431	2	US-09-038-832-2
13	130.5	8.2	431	2	US-09-038-832-4
14	130.5	8.2	447	2	US-09-949-016-8211
15	119	7.5	341	2	US-09-336-536-28
16	114	7.2	370	1	US-08-979-424-1
17	114	7.2	390	2	US-09-907-794A-39
18	114	7.2	390	2	US-09-905-125A-39
19	114	7.2	390	2	US-09-902-775A-39
20	114	7.2	390	2	US-09-906-700-39
21	114	7.2	390	2	US-09-903-603A-39
22	114	7.2	390	2	US-09-904-920A-39
23	114	7.2	390	2	US-09-909-064-39
24	114	7.2	390	2	US-09-905-381A-39
25	114	7.2	390	2	US-09-906-618-39
26	114	7.2	390	2	US-09-906-646-39
27	114	7.2	390	2	US-09-906-646-39

28	114	7.2	390	2	US-09-904-462-39	Sequence 39, Appl
29	114	7.2	390	2	US-09-902-736A-39	Sequence 39, Appl
30	114	7.2	390	2	US-09-906-722A-39	Sequence 39, Appl
31	114	7.2	417	2	US-09-949-016-6729	Sequence 6729, Ap
32	114	7.2	456	2	US-09-949-016-7564	Sequence 7564, Ap
33	113.5	7.1	319	1	US-08-597-495B-22	Sequence 22, Appl
34	113.5	7.1	319	2	US-09-068-051A-22	Sequence 22, Appl
35	113.5	7.1	319	2	US-09-336-536-67	Sequence 67, Appl
36	113.5	7.1	319	2	US-09-254-465A-6	Sequence 6, Appl
37	113.5	7.1	319	2	US-09-953-499-6	Sequence 6, Appl
38	113	7.1	316	2	US-09-397-243D-13	Sequence 13, Appl
39	111.5	7.0	306	2	US-09-369-247-63	Sequence 63, Appl
40	111.5	7.0	306	2	US-10-062-548-63	Sequence 63, Appl
41	110.5	6.9	244	2	US-08-918-148-79	Sequence 79, Appl
42	110.5	6.9	244	2	US-09-138-091A-77	Sequence 77, Appl
43	110	6.9	300	1	US-08-661-052-4	Sequence 4, Appl
44	110	6.9	300	2	US-09-188-082-4	Sequence 4, Appl
45	110	6.9	300	2	US-09-364-088-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-985-950-2
; Sequence 2, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-950-2

Query Match 100.0%; Score 1591; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.5e-141;

Matches	303;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	1	MGRPLLLPLLLPAPFLQPSGTS	GGPSYLYGV	TQPKHLSASMG	SGSVI	PPSPFY	PWE	60	
Qy	61	LATAPDVRI	SWRRGHFHGQSFYSTR	PPSIHKDYVNR	FLFNWTEGQ	SGFLRIS	NLQKQD	120	
Db	61	LATAPDVRI	SWRRGHFHGQSFYSTR	PPSIHKDYVNR	FLFNWTEGQ	SGFLRIS	NLQKQD	120	
Qy	121	SVYFCRVELD	TRSGRGQWOSI	EGTKLSI	IQAVTTTT	QRPSSMTT	WRLS	TTTTTGLRV	180
Db	121	SVYFCRVELD	TRSGRGQWOSI	EGTKLSI	IQAVTTTT	QRPSSMTT	WRLS	TTTTTGLRV	180
Qy	181	TQGRSDS	WHISLETAVG	VAVAVTV	IGIMILGI	CILRRRRK	GQORTKAT	TAREP	PFQ 240
Db	181	TQGRSDS	WHISLETAVG	VAVAVTV	IGIMILGI	CILRRRRK	GQORTKAT	TAREP	PFQ 240
Qy	241	NTEEPYENIR	NEQNTD	PKLNPK	DDGIVYAS	LALSSST	SPRPPSHR	PLKSPQNETI	YSV 300
Db	241	NTEEPYENIR	NEQNTD	PKLNPK	DDGIVYAS	LALSSST	SPRPPSHR	PLKSPQNETI	YSV 300
Qy	301	LKA	303						
Db	301	LKA	303						

RESULT 2

US-09-546-049-2
/ Sequence 2, Application US/09546049
/ Patent No. 6479638
/ GENERAL INFORMATION:
/ APPLICANT: Adema, Gosse Jan
/ Meyaard, Linde
/ Gorman, Daniel M.
/ McClanahan, Terrill K.
/ Zurawski, Sandra M.
/ Zurawski, Gerard
/ Lanier, Lewis L.
/ Phillips Jr., Joseph H.
/ TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
/ Related Reagents

RESULT 3
US-09-869-388-2
; Sequence 2. Application US/09869388

Query Match	100.0%;	Score 1591;	DB 2;	Length 303;
Best Local Similarity	100.0%;	Pred. No. 1.5e-14;		
Matches 303;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	1	MGRPLLLPLLLPLPAFLQPSGSTGSPSYLVGVTPKHLASMGSGSVEIPSPFYYPWE	60
Qy	61	LATAPDVRISWRGHPHGQSFYSTRPPSIHKQVYNFLFNLTWTEGQSGGFLRISLNKQDQ	120
Db	61	LATAPDVRISWRGHPHGQSFYSTRPPSIHKQVYNFLFNLTWTEGQSGGFLRISLNKQDQ	120
Qy	121	SVYFCRVELDTRSSGRQWQSGTEGKLSITQAVTTTTTORPSSMTTWRLSSTTTTTTGLRV	180

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 103.088 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-2

Perfect score: 1591

Sequence: 1 MGRPELLLPPLLPPLPAPLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1591	100.0	303	3	US-09-774-381-58
2	1591	100.0	303	4	US-10-290-631-2
3	1591	100.0	303	4	US-10-780-043-2
4	1591	100.0	303	5	US-10-777-524-2
5	1591	100.0	303	5	US-10-777-521-2
6	1176.5	73.9	230	4	US-10-780-043-4
7	1171.5	73.6	230	4	US-10-309-290-110
8	1010.5	63.5	206	4	US-10-309-290-112
9	973.5	61.2	226	3	US-09-774-381-44
10	973.5	61.2	226	4	US-10-780-043-10
11	967.5	60.8	227	3	US-09-745-763-106
12	958	60.2	227	4	US-10-262-445-128
13	958	60.2	227	4	US-10-780-043-6
14	958	60.2	227	5	US-10-820-474A-7
15	958	60.2	291	3	US-09-935-390A-21
16	958	60.2	326	4	US-10-276-774-2380
17	934	58.7	238	3	US-09-809-391-485
18	934	58.7	238	3	US-09-882-171-485
19	934	58.7	238	4	US-10-164-861-485
20	821	51.6	175	4	US-10-780-043-8
21	808	50.8	1012	5	US-10-450-763-30868
22	808	50.8	1012	5	US-10-450-763-33210
23	808	50.8	1012	5	US-10-450-763-47228
24	808	50.8	1012	5	US-10-450-763-51762
25	517	32.5	101	3	US-09-809-391-754
26	517	32.5	101	3	US-09-882-171-754
27	517	32.5	101	4	US-10-164-861-754

28	411	25.8	224	3	US-09-866-050A-711	Sequence 711, App
29	222	14.0	99	4	US-10-290-631-4	Sequence 4, Appli
30	222	14.0	99	4	US-10-777-524-4	Sequence 4, Appli
31	222	14.0	99	5	US-10-777-521-4	Sequence 4, Appli
32	148.5	9.3	305	4	US-10-291-265-391	Sequence 391, App
33	148.5	9.3	305	5	US-10-727-012-3	Sequence 3, Appli
34	148.5	9.3	305	5	US-10-962-127-3	Sequence 3, Appli
35	148.5	9.3	305	5	US-10-962-127-58	Sequence 58, Appli
36	146.5	9.2	305	3	US-09-796-753-104	Sequence 104, App
37	146.5	9.2	305	3	US-09-796-753-120	Sequence 120, App
38	146.5	9.2	305	4	US-10-291-265-863	Sequence 863, App
39	139	8.7	290	3	US-09-965-529-18	Sequence 18, Appl
40	139	8.7	290	3	US-09-969-680A-18	Sequence 18, Appl
41	139	8.7	290	4	US-10-227-884-40	Sequence 40, Appl
42	139	8.7	290	4	US-10-230-163-40	Sequence 40, Appl
43	139	8.7	290	4	US-10-230-338-40	Sequence 40, Appl
44	139	8.7	290	4	US-10-218-631-40	Sequence 40, Appl
45	139	8.7	290	4	US-10-230-414-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-09-774-381-58
; Sequence 58, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL EDIFR, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; FILE REFERENCE: MNI-107CF2
; CURRENT APPLICATION NUMBER: US/09/774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-381-58

Query Match 100.0%; Score 1591; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.6e-126;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPELLLPPLLPPLPAPLQSGPSVLYGVYTOPKHLASMGGSVEIPFSYVYDRE 60
|||||

Db 1 MGRPLLLPLLLPPAFLOPSGSGPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60
QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLNLTWTEQKSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLNLTWTEQKSGFLRISNLQKQDQ 120
QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSSMTTWRSLSTTTTGLRV 180
Db 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSSMTTWRSLSTTTTGLRV 180
QY 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKGOQRTKATTPAREPFQ 240
Db 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKGOQRTKATTPAREPFQ 240
QY 241 NTEEPYENIRNEGQNTDPKLPKDDGIVYASLALSSSTSPRAPPSPKSPQNETLYSV 300
Db 241 NTEEPYENIRNEGQNTDPKLPKDDGIVYASLALSSSTSPRAPPSPKSPQNETLYSV 300
QY 301 LKA 303
Db 301 LKA 303

RESULT 2

US-10-290-631-2

; Sequence 2, Application US/10290631

; Publication No. US20030105303A1

GENERAL INFORMATION:

APPLICANT: Adema, Gosse Jan

Meygaard, Linde

Gorman, Daniel M.

McClanahan, Terrill K.

Zurawski, Sandra M.

Zurawski, Gerard

Lanier, Lewis L.

Phillips Jr., Joseph H.

TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;

Related Reagents

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/290,631

FILING DATE: 08-NO. US20030105303A1-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/985,950

FILING DATE: 05-DEC-1997

APPLICATION NUMBER: US 60/041,279

FILING DATE: 21-MARCH-1997

APPLICATION NUMBER: US 60/033,181

FILING DATE: 16-DEC-1996

APPLICATION NUMBER: US 60/032,252

FILING DATE: 06-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0670K

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)852-9196

TELEFAX: (650)496-1204

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-290-631-2

Query Match 100.0%; Score 1591; DB 4; Length 303;

Best Local Similarity 100.0%; Pred. No. 6.6e-126;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLLLPPAFLOPSGSGPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60

Db 1 MGRPLLLPLLLPPAFLOPSGSGPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60

QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLNLTWTEQKSGFLRISNLQKQDQ 120

Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLNLTWTEQKSGFLRISNLQKQDQ 120

QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSSMTTWRSLSTTTTGLRV 180

Db 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSSMTTWRSLSTTTTGLRV 180

QY 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKGOQRTKATTPAREPFQ 240

Db 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKGOQRTKATTPAREPFQ 240

QY 241 NTEEPYENIRNEGQNTDPKLPKDDGIVYASLALSSSTSPRAPPSPKSPQNETLYSV 300

Db 241 NTEEPYENIRNEGQNTDPKLPKDDGIVYASLALSSSTSPRAPPSPKSPQNETLYSV 300

QY 301 LKA 303

Db 301 LKA 303

RESULT 3

US-10-780-043-2

; Sequence 2, Application US/10780043

; Publication No. US20040137506A1

; GENERAL INFORMATION:

; APPLICANT: Bates, Elizabeth

; APPLICANT: Fournier, Nathalie

; APPLICANT: Chalus, Lionel

; APPLICANT: Garrone, Pierre

; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

; FILE REFERENCE: SF0977X

; CURRENT APPLICATION NUMBER: US/10/780,043

; CURRENT FILING DATE: 2004-02-17

; PRIOR APPLICATION NUMBER: US/09/869,388

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: IBM PC compatible

; SEQ ID NO 2

; LENGTH: 303

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-780-043-2

Query Match

Best Local Similarity 100.0%; Score 1591; DB 4; Length 303;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLLLPPAFLOPSGSGPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60

Db 1 MGRPLLLPLLLPPAFLOPSGSGPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60

QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLNLTWTEQKSGFLRISNLQKQDQ 120

Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLNLTWTEQKSGFLRISNLQKQDQ 120

QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSSMTTWRSLSTTTTGLRV 180

Result No.	Query #				DB	ID	Description
	Score	Match	Length				
1	148.5	9.3	305	7	US-11-000-463-391	Sequence 391, App	
2	146.5	9.2	305	7	US-11-000-463-863	Sequence 863, App	
3	121	7.6	406	7	US-11-000-463-377	Sequence 377, App	
4	121	7.6	406	7	US-11-000-463-849	Sequence 849, App	
5	114	7.2	390	6	US-10-131-826A-338	Sequence 338, App	
6	112.5	7.1	258	6	US-10-512-184-26	Sequence 26, App	
7	112.5	7.1	327	6	US-10-512-184-62	Sequence 62, App1	
8	112.5	7.1	327	6	US-10-512-184-64	Sequence 64, App1	
9	112.5	7.1	328	6	US-10-512-184-63	Sequence 63, App1	
10	112.5	7.1	576	6	US-10-512-184-65	Sequence 65, App1	
11	112.5	7.1	625	6	US-10-512-184-47	Sequence 47, App1	
12	110.5	6.9	246	7	US-11-054-515-2077	Sequence 2077, App	
13	110.5	6.9	246	7	US-11-054-515-2079	Sequence 2079, App	
14	108.5	6.8	256	7	US-11-054-515-907	Sequence 907, App1	
15	106.5	6.7	250	6	US-10-512-184-27	Sequence 27, App1	
16	106	6.7	250	7	US-11-054-515-1319	Sequence 1319, App	
17	106	6.7	258	7	US-11-054-515-1841	Sequence 1841, App	
18	104	6.5	231	7	US-11-000-463-283	Sequence 283, App	
19	104	6.5	348	7	US-11-174-150-33	Sequence 33, App1	
20	104	6.5	488	6	US-10-995-561-860	Sequence 860, App	
21	104	6.5	551	7	US-11-000-463-345	Sequence 346, App	
22	104	6.5	727	6	US-10-995-561-864	Sequence 864, App	
23	104	6.5	847	6	US-10-995-561-865	Sequence 863, App	
24	104	6.5	847	6	US-10-995-561-865	Sequence 865, App	
25	103.5	6.5	246	7	US-11-054-515-1589	Sequence 1589, App	

Db 1 MLLTLTLLFWL-----SGYIVTQITGPTTVNGLRGLSLVQCVRSGMWETYLK-- 51
QY 67 VRISWRGHPHQGFYSTRPPSIHKDYVNRFLNWTGQKSGFLRIS--NLQKQDSVYF 124
Db 52 ---WRCGAIWRDCKILVKTSGSEQE-VKRDVSIKDNQKRTFTVTMEDLMKTDADTYW 107
QY 125 CRVELDTRSSGRQWOSIEGTKLSITQAVT---TTQRPSSMTTW-----RLSSTT 173
Db 108 CGIEK-----TGNDLGVTVQVITDPASTPAPTPTTFTTAPVQETSSSP 154
QY 174 TTTGLRVTOGKRSDSWHISLETAVGAVAVATVGLIMILGLICLLRWRKGGQORTKATT 233
Db 155 TLTG-----HHLDRHKLKLSVLLPLIFTIL-LLLLVAASLLAWRMKYOQKAAGMS 206
QY 234 PAR--EPQNTTEBYENIRNEGQNTDP-----KLN-----PKDDGIVY 269
Db 207 PEQVLQPLEG-DLCYADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMASLPKED-ISKY 264
QY 270 ASIALSSSTSPRAP-----PSHRPLKSPQNETLYSVL 301
Db 265 ASLTIGA--EDQEPYCNMGLSHSLPGRGPPEPTEYSTI 302

RESULT 2

US-11-000-463-863
; Sequence 863, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 863
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-863

Query Match 9.2%; Score 146.5; DB 7; Length 305;
Best Local Similarity 23.5%; Pred. No. 7.6e-06;
Matches 80; Conservative 51; Mismatches 126; Indels 83; Gaps 16;
QY 7 LPLPLLLPAPFLOPQSGTSGPSYLYGVTOPKHLASMGSGSVIPIPSFYFVWELATPD 66
Db 1 MLLTLTLLFWL-----SGYIVTQITGPTTVNGLRGLSLVQCVRSGMWETYLK-- 51

QY 67 VRISWRGHPHQGFYSTRPPSIHKDYVNRFLNWTGQKSGFLRIS--NLQKQDSVYF 124
Db 52 ---WRCGAIWRDCKILVKTSGSEQE-VKRDVSIKDNQKRTFTVTMEDLMKTDADTYW 107
QY 125 CRVELDTRSSGRQWOSIEGTKLSITQAVT---TTQRPSSMTTW-----RLSSTT 173
Db 108 CGIEK-----TGNDLGVTVQVITDPASTPAPTPTTFTTAPVQETSSSP 154
QY 174 TTTGLRVTOGKRSDSWHISLETAVGAVAVATVGLIMILGLICLLRWRKGGQORTKATT 233
Db 155 TLTG-----HHLDRHKLKLSVLLPLIFTIL-LLLLVAASLLAWRMKYOQKAAGMS 206
QY 234 PAR--EPQNTTEBYENIRNEGQNTDP-----KLN-----PKDDGIVY 269
Db 207 PEQVLQPLEG-DLCYADLTQLAGTSRKATTKLSSAQVDQVEVEYVTMASLPKED-ISKY 264
QY 270 ASIALSSSTSPRAP-----PSHRPLKSPQNETLYSVL 301
Db 265 ASLTIGA--EDQEPYCNMGLSHSLPGRGPPEPTEYSTI 302

RESULT 3

US-11-000-463-377
; Sequence 377, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 377
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-377

Query Match 7.6%; Score 121; DB 7; Length 406;
Best Local Similarity 24.7%; Pred. No. 0.0017;
Matches 74; Conservative 37; Mismatches 130; Indels 58; Gaps 13;
QY 5 LLLPLLLPAPFLOPQSGTSGPSYLYGVTOPKHLASMGSGSVIPIPSFYFVWELATA 64
Db 3 LLLPLLLPMTGKME--GDRQYGDGYLLQVQZ--LVTQVGLCVHVPSCSFSYPQDQWTD 58
QY 65 PD-VRISWRGHPHQGFYSTRPPSIHKDYVNRFLNWTGQ-----KSGFLRIS 114

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	144.5	9.1	823	2	S48394	probable membrane
2	123.5	7.8	1114	2	T49517	p63 related protei
3	118.5	7.4	509	2	JC5288	SHP substrate-1 pr
4	116	7.3	392	2	B44194	poliiovirus recepto
5	116	7.3	417	2	A44194	poliiovirus recepto
6	115.5	7.3	513	2	JC5289	SHP substrate-1 pr
7	114	7.2	392	1	RWHUPD	poliiovirus recepto
8	114	7.2	417	1	RWHUPA	poliiovirus recepto
9	112.5	7.1	403	2	I52590	m33-B isoform - mo
10	110	6.9	235	2	I52598	Ig lambda chain -
11	110	6.9	847	2	JH0371	B-cell adhesion pr
12	109.5	6.9	233	2	S25747	Ig lambda chain -
13	108.5	6.8	230	2	S49449	Ig lambda chain -
14	108.5	6.8	235	2	S14675	Ig lambda chain -
15	108.5	6.8	862	2	I49583	differentiation an
16	108.5	6.8	868	2	A46512	CD22 homolog/B lym
17	108	6.8	236	2	S25746	Ig lambda chain -
18	108	6.8	1694	2	S50065	sialoadhesin - mou
19	106	6.7	647	2	A35488	B-cell adhesion pr
20	106	6.7	710	2	A39486	ABC transporter, b
21	105.5	6.6	235	2	S25750	Ig lambda chain -
22	104.5	6.6	214	2	PC4156	Ig lambda chain v
23	104	6.5	231	2	S25751	Ig lambda chain -
24	104	6.5	798	2	T34248	hypothetical prote
25	103	6.5	446	2	T45525	WSC4 homolog [limp
26	103	6.5	469	2	S37483	Ig gamma-2a chain
27	102.5	6.4	407	2	T08732	hypothetical prote
28	102	6.4	572	2	B46529	Ig Y heavy chain (
29	101	6.3	118	2	E27889	Ig heavy chain v

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 130.752 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-2
Perfect score: 1591
Sequence: 1 MGRPLLLPPLPPAPFLQ.....PSHRPLKSPQNETLYSLVLA 303

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1588	99.8	303	Q9UKJ1_HUMAN	Q9ukj1 homo sapien
2	997.5	62.7	226	Q8NH11_HUMAN	Q8nh11 homo sapien
3	958	60.2	227	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
4	630	39.6	299	Q8BYA6_MOUSE	Q8bya6 mus musculus
5	144.5	9.1	823	AXL2_YEAST	P38928 saccharomyc
6	139	8.7	290	Q6UX24_HUMAN	Q6ux24 homo sapien
7	139	8.7	290	Q726A6_HUMAN	Q726a6 homo sapien
8	136	8.5	290	Q8TDQ1_HUMAN	Q8tdq1 homo sapien
9	135.5	8.5	293	Q727I5_HUMAN	Q727i5 homo sapien
10	130.5	8.2	499	SIGL8_HUMAN	Q9ny24 homo sapien
11	130	8.2	289	Q6OX35_MOUSE	Q6ox36 mus musculus
12	129.5	8.1	233	Q8TEC9_HUMAN	Q8tbc9 homo sapien
13	127	8.0	283	Q5DNW6_EPTBU	Q5dwn6 eptatretus
14	123.5	7.8	328	Q6ZMC9_HUMAN	Q6zmc9 homo sapien
15	123.5	7.8	353	Q5TDQ5_NEUCR	Q5tdq5 neurospora
16	123.5	7.8	858	Q5VT77_BRARE	Q5vtv7 brachydanio
17	122.5	7.7	235	Q9SM11_MOUSE	Q9sm11 mus musculus
18	122	7.7	288	Q46707_FUGRU	Q46707 fugu rubrip
19	122	7.7	367	Q4GUE4_FUGRU	Q4gje4 fugu rubrip
20	121.5	7.6	633	Q5W434_BRARE	Q5w434 brachydanio
21	121.5	7.6	651	Q5W433_BRARE	Q5w433 brachydanio
22	120	7.5	236	Q6PIQ7_HUMAN	Q6piq7 homo sapien
23	120	7.5	283	Q5DMN5_EPTBU	Q5dwn5 eptatretus
24	119.5	7.5	434	Q872V2_NEUCR	Q872v2 neurospora
25	119	7.5	318	Q9IB03_9PERC	Q9ib03 spheeroides
26	117.5	7.4	235	Q6P2J1_HUMAN	Q6p2j1 homo sapien
27	117.5	7.4	366	Q46705_FUGRU	Q46705 fugu rubrip
28	116	7.3	417	PVR_CBRAE	P32506 cercopithec
29	115.5	7.3	513	SHP51_MOUSE	P97797 m tyrosine-
30	115	7.2	367	Q46706_FUGRU	Q46706 fugu rubrip
31	114.5	7.2	235	Q6P790_HUMAN	Q6p790 homo sapien

32	114.5	7.2	283	Q5DMN4_EPTBU	Q5dwn4 eptatretus
33	114	7.2	390	ESAM_HUMAN	Q96ap7 homo sapien
34	114	7.2	417	PVR_HUMAN	P15151 homo sapien
35	113.5	7.1	319	GPA33_HUMAN	Q99795 homo sapien
36	113.5	7.1	319	Q5VZP6_HUMAN	Q5vzp6 homo sapien
37	113.5	7.1	387	SIG13_PANTR	Q64ja4 pan troglod
38	113	7.1	283	Q5DMN2_EPTBU	Q5dwn2 eptatretus
39	113	7.1	401	Q88835_CERAE	Q88835 cercopithec
40	113	7.1	718	O73675_XENLA	O73675 xenopus lae
41	113	7.1	718	Q6PCK4_XENLA	Q6pck4 xenopus lae
42	112.5	7.1	403	CD33_MOUSE	Q63994 mus musculus
43	112.5	7.1	700	Q8TG00_ASPFU	Q8tg00 aspergillus
44	112.5	7.1	700	O4WS89_ASPFU	O4ws89 aspergillus
45	112.5	7.1	1795	O76894_DROME	O76894 drosophila

ALIGNMENTS

RESULT 1
ID Q9UKJ1_HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PILRBeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD52964.1; -; mRNA.
DR Ensembl; ENSG0000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; P:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;

Query Match	99.8%;	Score 1588;	DB 2;	Length 303;
Best Local Similarity	99.7%;	Pred. No. 9.3e-124;		
Matches 302;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGRPLLLPPLLPAPFLQPSGTSGPSYLVGVTPKHLASMSGSGVEIPFSFYYPWE	60	
Db	1	MGRPLLLPPLLPAPFLQPSGTSGPSYLVGVTPKHLASMSGSGVEIPFSFYYPWE	60	
QY	61	LATAPDVRIWRRGHFGHQSFYSTRPPSIHKDYVNRFLFNWTGQKSGFLRISLNKQDQ	120	
Db	61	LATAPDVRIWRRGHFGHQSFYSTRPPSIHKDYVNRFLFNWTGQKSGFLRISLNKQDQ	120	
QY	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPQSSMTTWRLSSITTTTGLRV	180	
Db	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPQSSMTTWRLSSITTTTGLRV	180	
QY	181	TQKRRSDSWHISLETAVGVAVTVLGMILGLICLLRWRRKGGQORTKATTPAREPFQ	240	
Db	181	TQKRRSDSWHISLETAVGVAVTVLGMILGLICLLRWRRKGGQORTKATTPAREPFQ	240	

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QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIYVASLSSSTSPRAPSHRPLKSPQNETLYSV 300
Db 241 NTEEPYENIRNEGQNTDPKLNPKDDGIYVASLSSSTSPRAPSHRPLKSPQNETLYSV 300
QY 301 LKA 303
Db 301 LKA 303

RESULT 2
ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH11;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PILRA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzhanovskii M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC017812; AAH17812.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;

Query Match 62.7%; Score 997.5; DB 2; Length 226;
Best Local Similarity 67.8%; Pred. No. 8.7e-75;
Matches 196; Conservative 6; Mismatches 10; Indels 77; Gaps 2;

QY 1 MGRPLLLPLLLPLPPALPQSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
Db 1 MGRPLLLPLLLPLPPALPQSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
QY 61 LATAPDVIRISRRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEGQSGFLRISNLKQDQ 120
Db 61 LATAPDVIRISRRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEGQSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGRQOQMSIEGTKLISITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
Db 121 SVYFCRVELDTRSSGRQOQMSIEGTKLISITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
QY 121 SVYFCRVELDTRSSGRQOQMSIEGTKLISITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

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Db 121 SVYFCRVELDTRSSGRQOQMSIEGTKLISITQAVTTTQRPSSMTTWRLSSTTTTGLRV 151
QY 181 TOGKRSDSDSWHISLETAVGVAVVTLGIMILGLICLLRWRKRGQORTKATTPAREPQ 240
Db 152 -----GQORTKATTPAREPQ 167
QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIYVASLSSSTSPRAPSHRPL 289
Db 168 NTEEPYENIRNEGQNTDPKLNPK-----LHLTOSTSQPPSPQEPPEPDPV 212

RESULT 3
ID Q9UKJ0 HUMAN PRELIMINARY; PRT; 227 AA.
AC Q9UKJ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Activating receptor PILRBeta (Hypothetical protein DKFZp434O079).
GN Name=DKFZp434O079;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRBeta, a novel immunoreceptor tyrosine-based inhibitory motif-
RT bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
RT paired with the truncated counterpart PILRBeta."
RL J. Biol. Chem. 275:4467-4474 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- INTERACTION:
CC O95870:BATS; NbExp=1; IntAct=EBI-347958, EBI-348517;
DR EMBL; AF161081; AAD52565.1; -; mRNA.
DR EMBL; AL834336; CAH10711.1; -; mRNA.
DR IntAct; Q9UKJ0; -.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain; Receptor.
SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60A57EF09 CRC64;

Query Match 60.2%; Score 958; DB 2; Length 227;
Best Local Similarity 80.8%; Pred. No. 1.7e-71;
Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

QY 1 MGRPLLLPLLLPLPPALPQSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
Db 1 MGRPLLLPLLLPLPPALPQSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
QY 61 LATAPDVIRISRRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEGQSGFLRISNLKQDQ 120
Db 61 LATAPDVIRISRRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEGQSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGRQOQMSIEGTKLISITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
Db 121 SVYFCRVELDTRSSGRQOQMSIEGTKLISITQAVTTTQRPSSMTTWRLSSTTTTGLRV 172
QY 181 TOGKRSDSDSWHISLETAVGVAVVTLGIMILGLICLLR---WRRRKQOQ 227

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